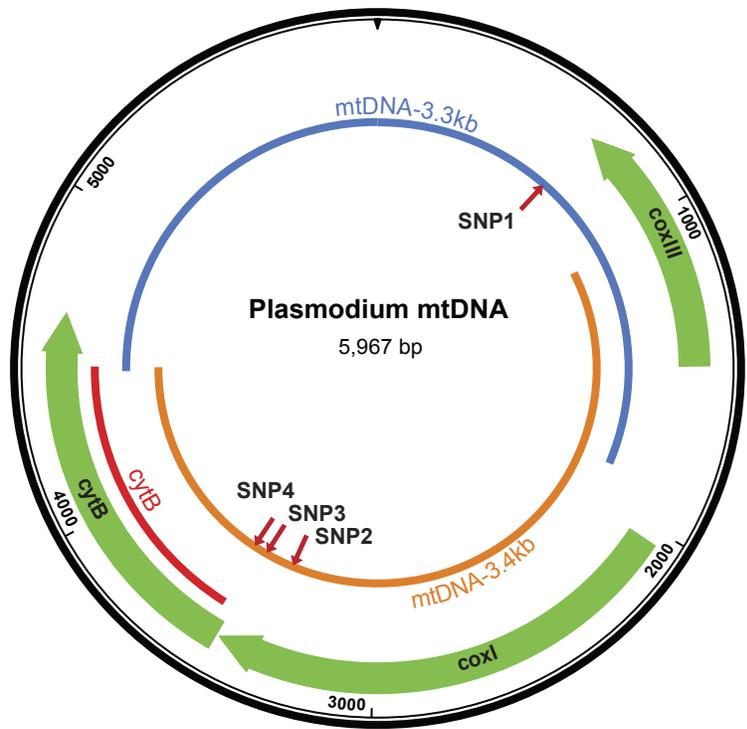
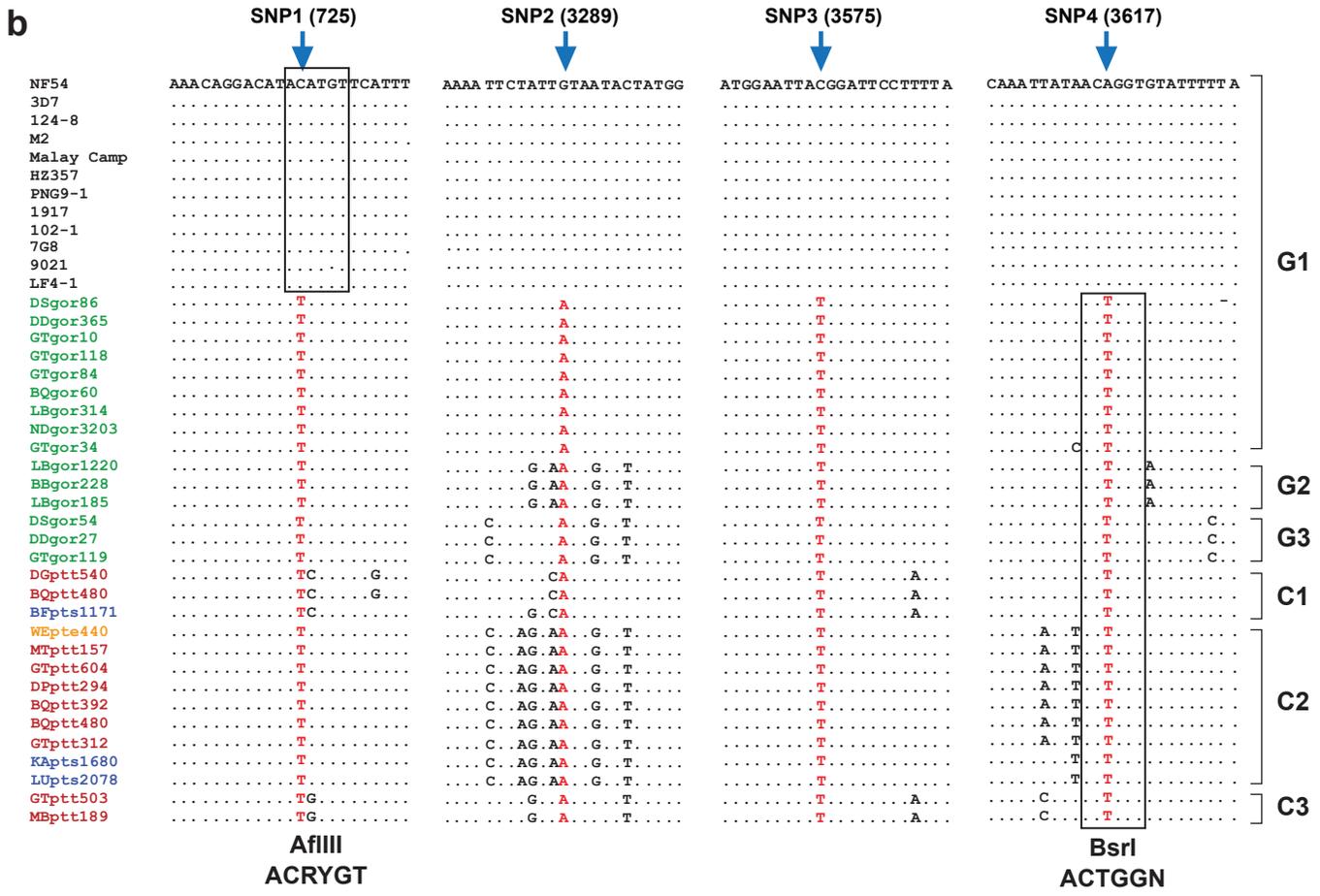


**a**



**b**



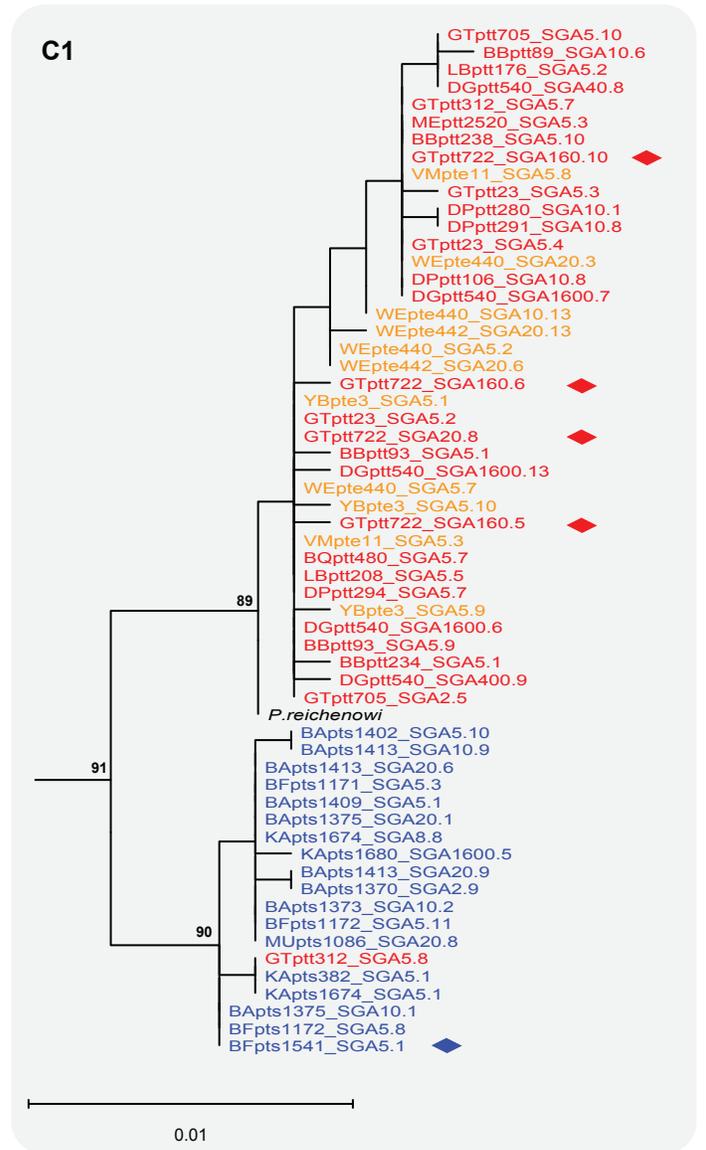
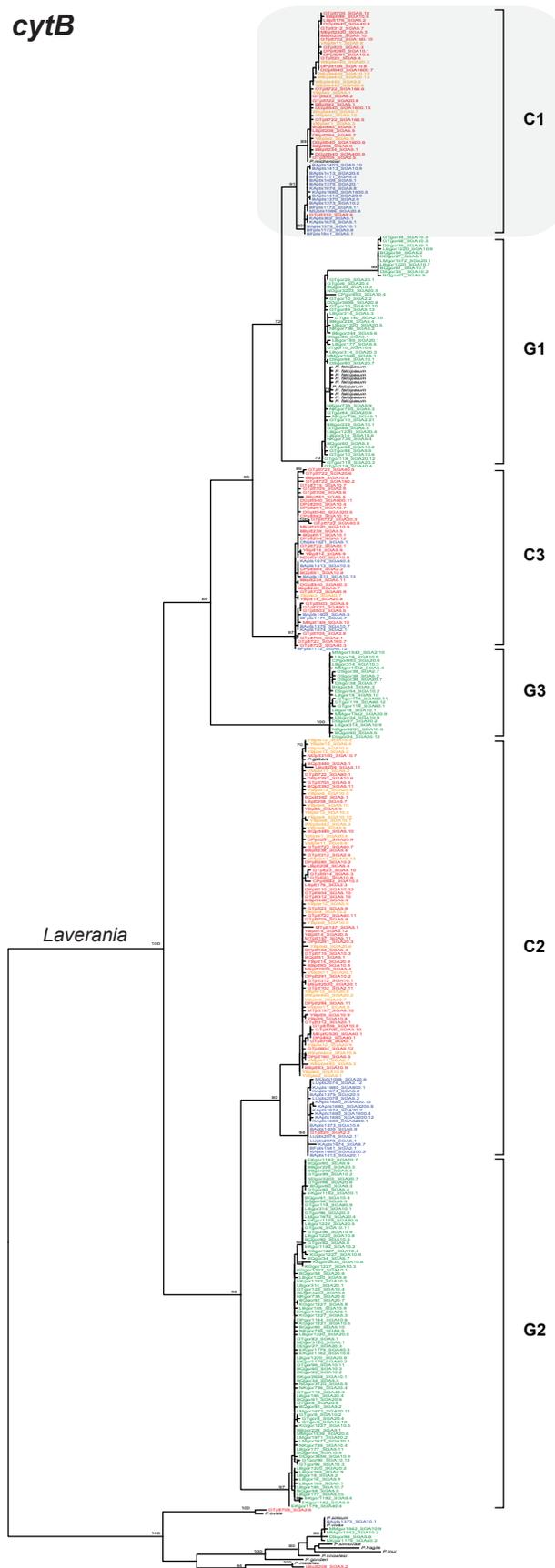
Supplementary Figure 1

**Supplementary Figure 1. Amplification of ape *Plasmodium* mitochondrial sequences for diagnostic and evolutionary studies.** **a**, Schematic representation of the *Plasmodium* mitochondrial genome. DNA fragments derived by diagnostic PCR (*cytB*), and/or single genome amplification (*cytB*, mtDNA-3.4kb, mtDNA-3.3kb) are shown in relation to cytochrome B (*cytB*), cytochrome C oxidase subunit I (*coxI*) and cytochrome C oxidase subunit III (*coxIII*) coding regions, respectively. The positions of four single nucleotide polymorphisms (SNP1-SNP4), which distinguish human *P. falciparum* from *Laverania* parasites, are also shown. **b**, Alignment of plasmidial mitochondrial sequences surrounding the SNPs depicted in (a). Representative members of the six *Laverania* species (G1-G3, C1-C3) are shown (see Supplementary Table 5 for all sequences available in these regions). Sequences are color-coded, with capital letters indicating the field site (Fig. 1) and lower case letters denoting the species and subspecies origin (ptt: *P. t. troglodytes*, red; pte: *P. t. ellioti*, orange; pts: *P. t. schweinfurthii*, blue; gor: *G. g. gorilla*, green). Sequences of human *P. falciparum* strains are shown in black (periods denote sequence identity with the NF54 reference sequence). Boxes highlight restriction enzyme recognition sites (*AflIII* and *BsrI*) that distinguish human *P. falciparum* and *Laverania* parasites. The position of the four SNPs (arrows) is indicated using NF54 for reference.



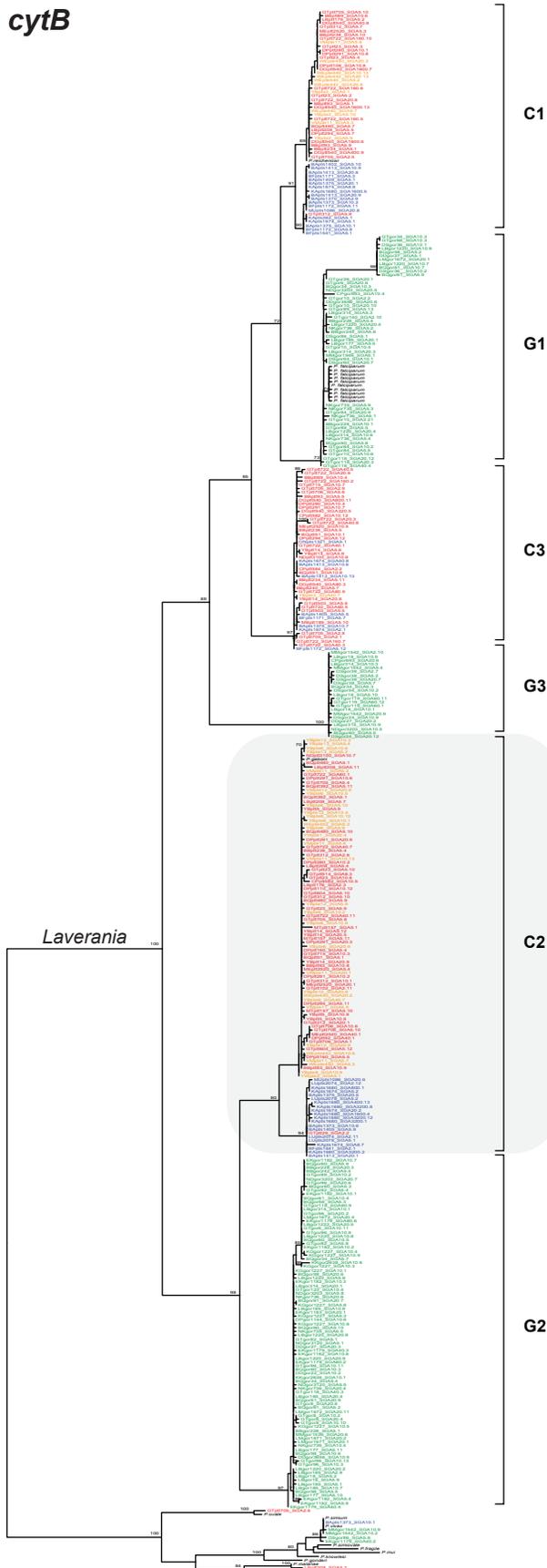
**Supplementary Figure 2. Phylogenetic tree of ape *Plasmodium* cytochrome B (*cytB*) sequences amplified by conventional (bulk) PCR.** Mitochondrial *cytB* (956 bp) sequences were amplified from 118 ape fecal samples using bulk PCR. Sequences are color-coded, with capital letters indicating the field site (Fig. 1) and lower case letters denoting the species and subspecies origin (ptt: *P. t. troglodytes*, red; pte: *P. t. ellioti*, orange; pts: *P. t. schweinfurthii*, blue; gor: *G. g. gorilla*, green). Arrows highlight replicate sequences from the same samples. Note that bulk PCR derived sequences obscured the existence of six distinct *Laverania* species that are clearly evident in trees from SGA derived sequences from the identical sample set (see Fig. 2 and Supplementary Fig. 3). Human and simian *Plasmodium* reference sequences are shown in black (see Supplementary Table 7 for GenBank accession numbers). The phylogenetic tree was inferred using PhyML<sup>30</sup> (the scale bar represents 0.01 substitutions per site).

cytB

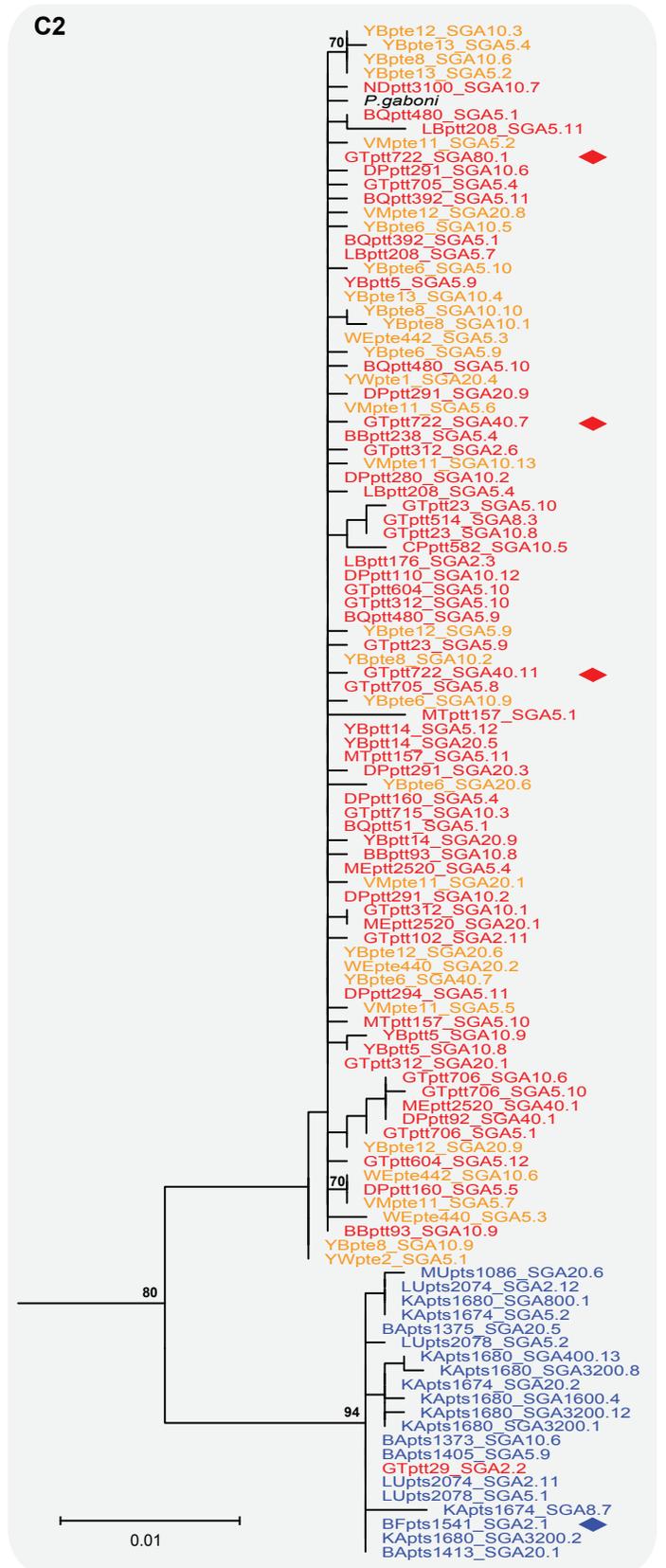


Supplementary Figure 3a

cytB

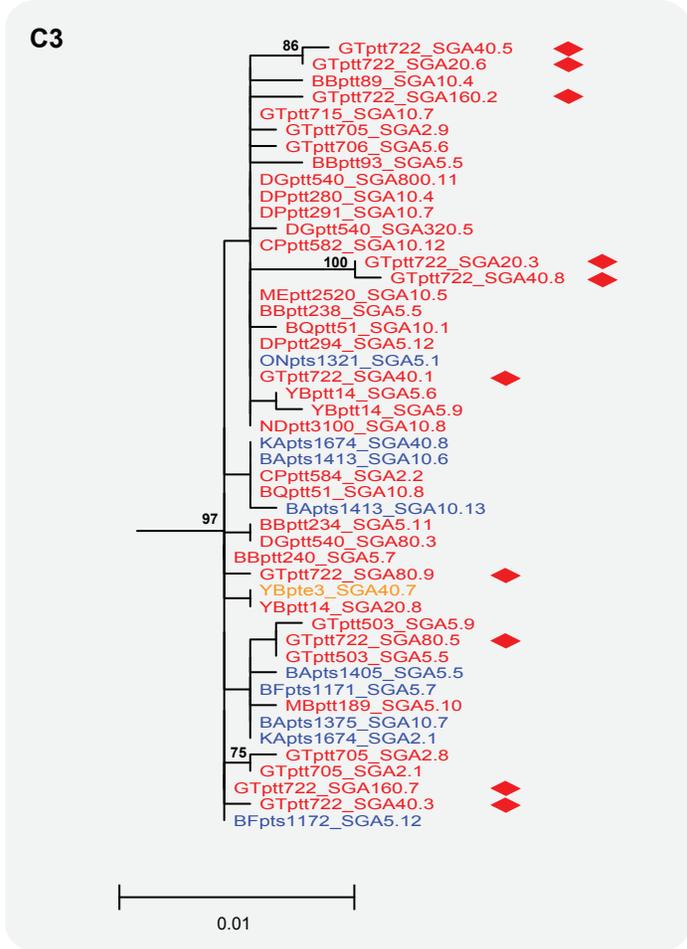
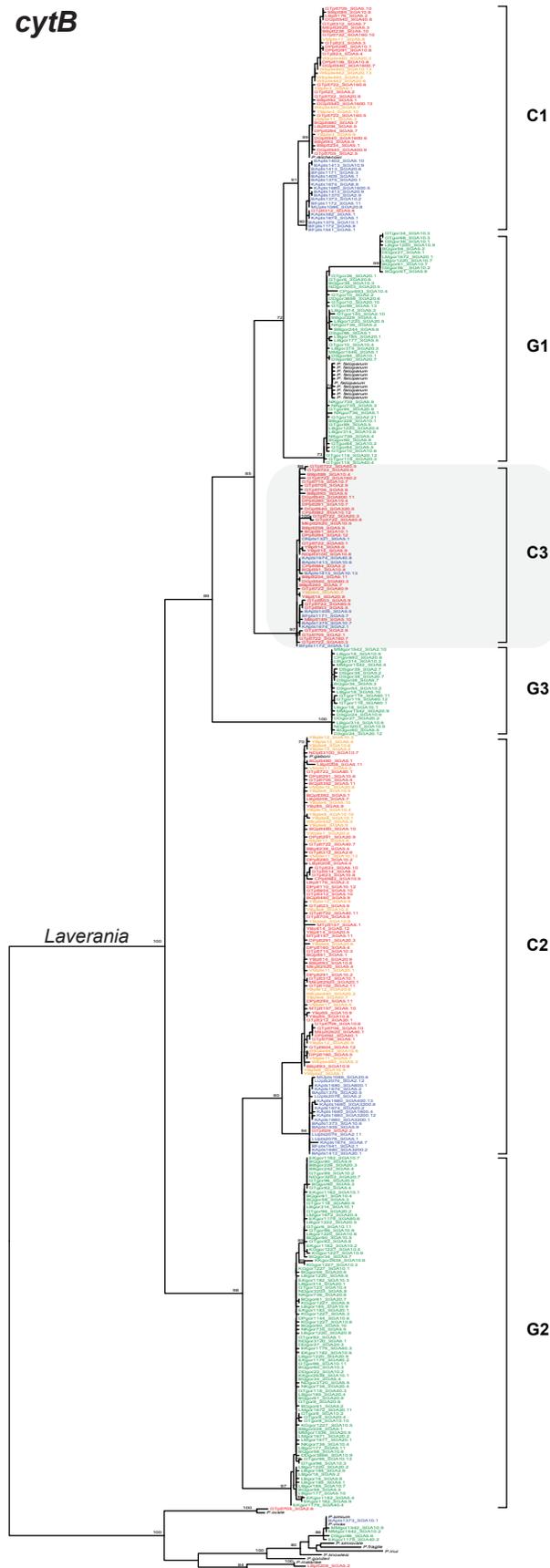


C2



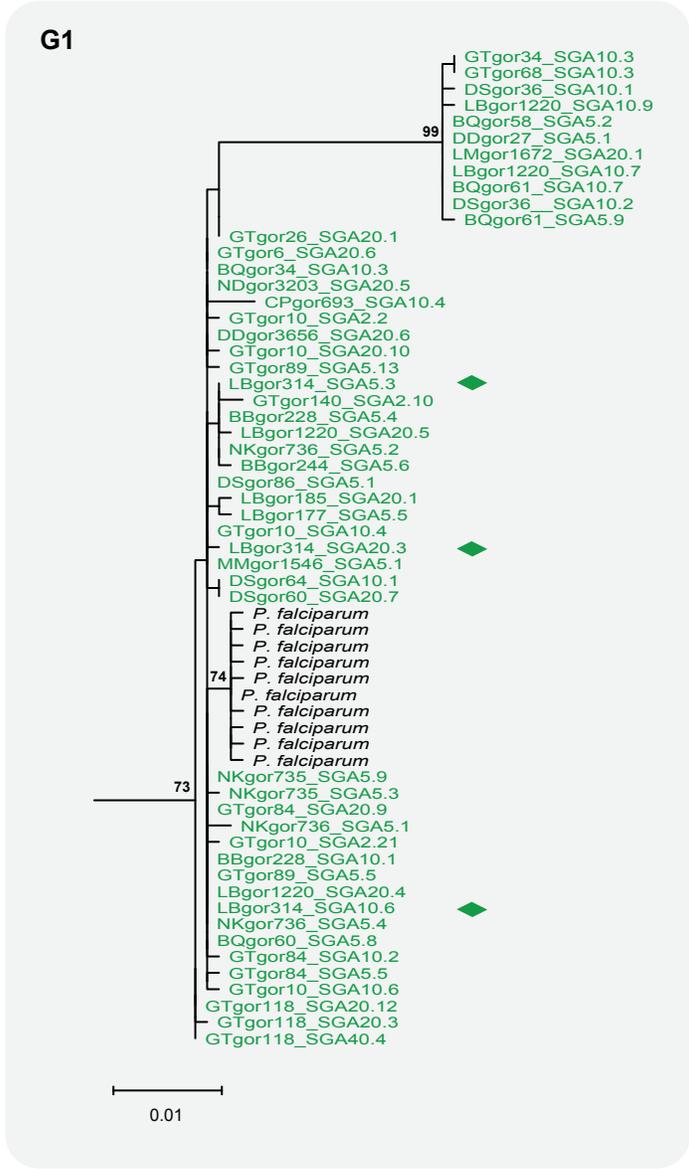
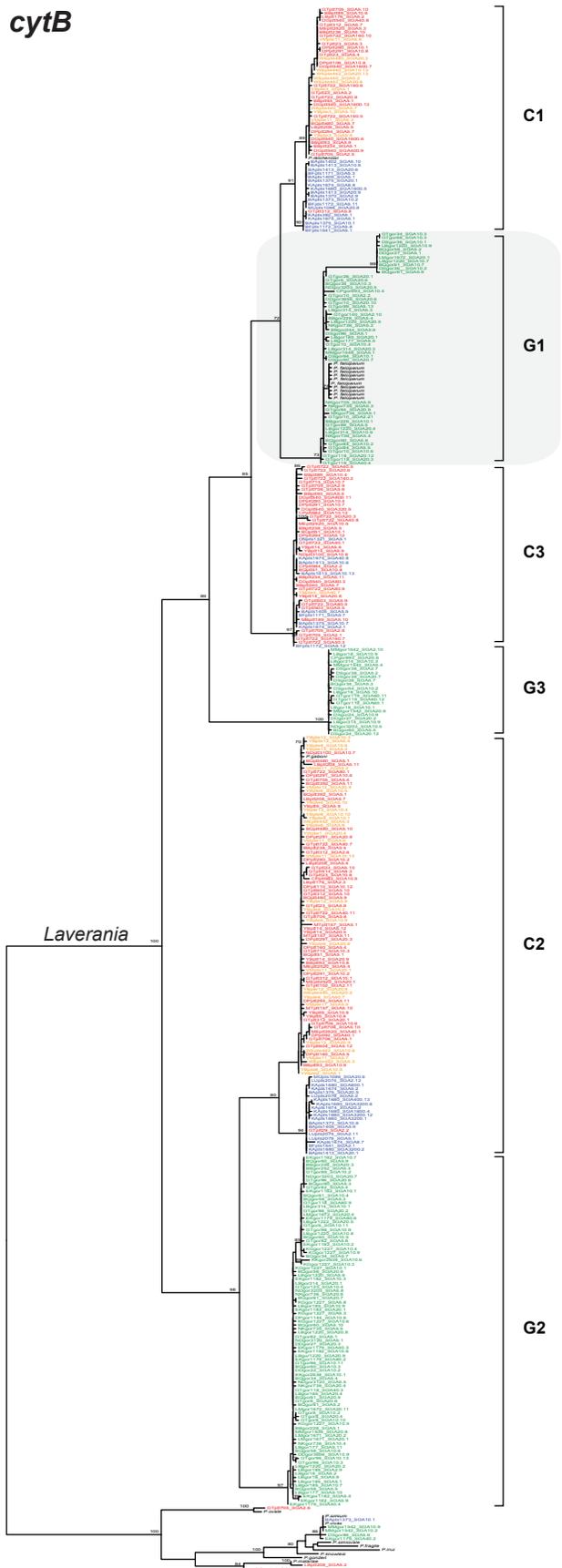
Supplementary Figure 3b

cytB



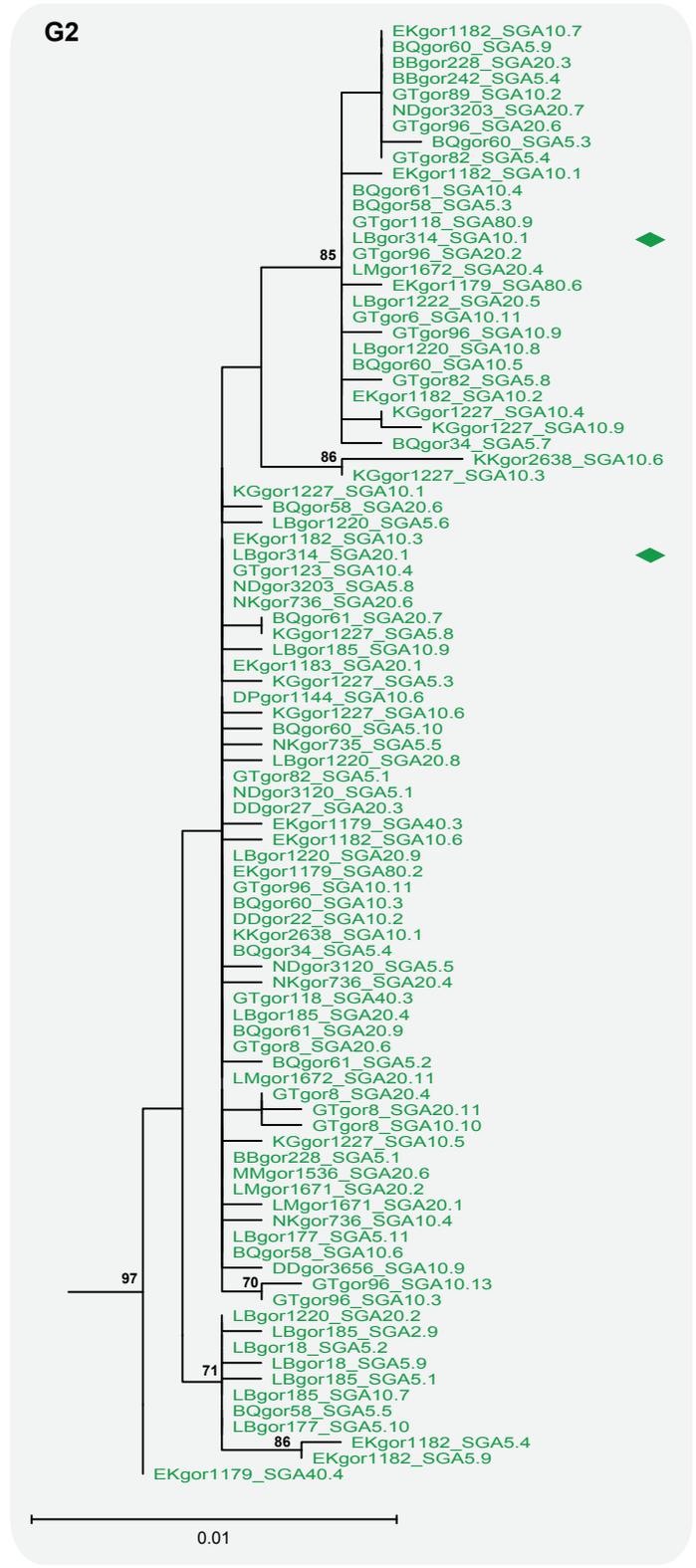
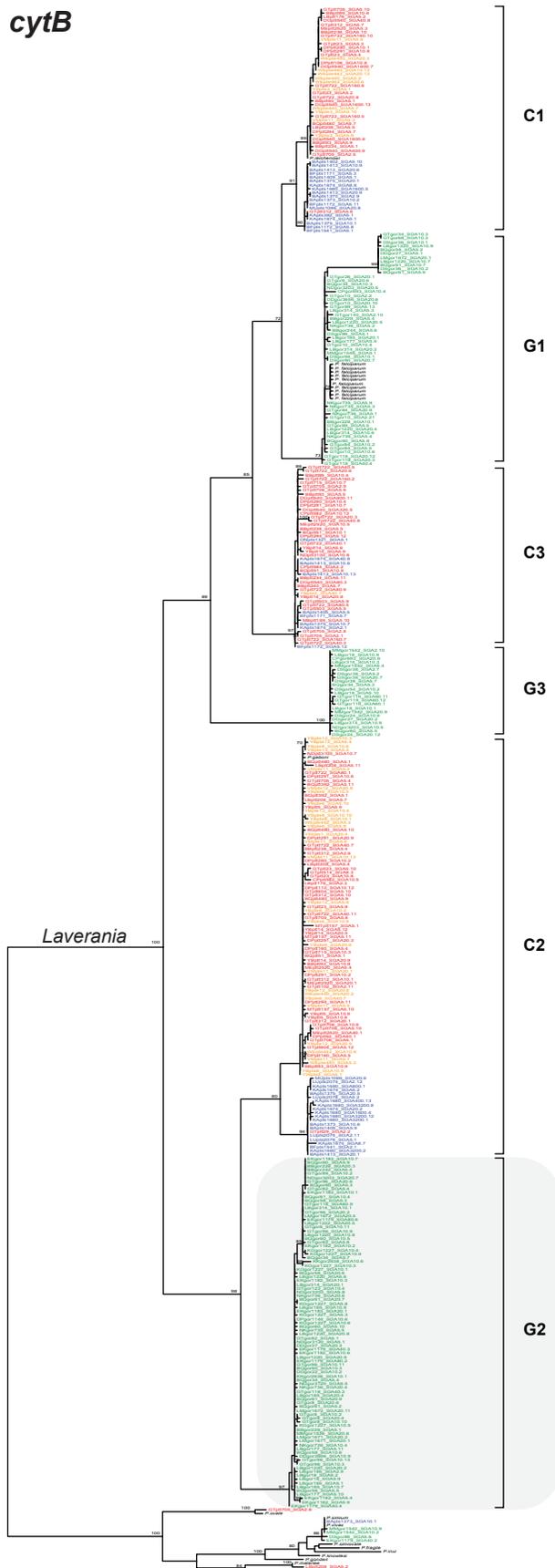
Supplementary Figure 3c

cytB



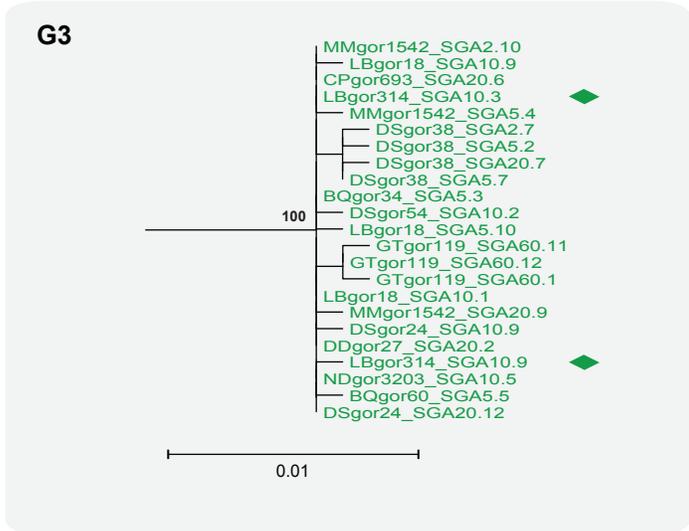
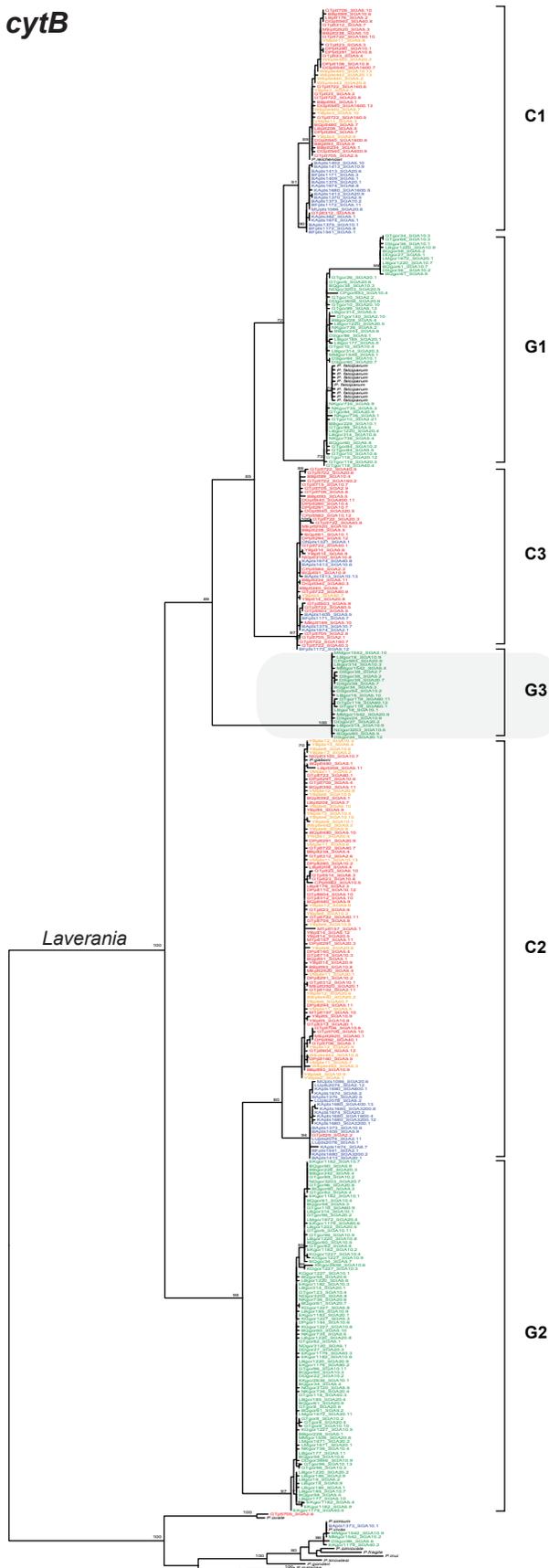
Supplementary Figure 3d

cytB



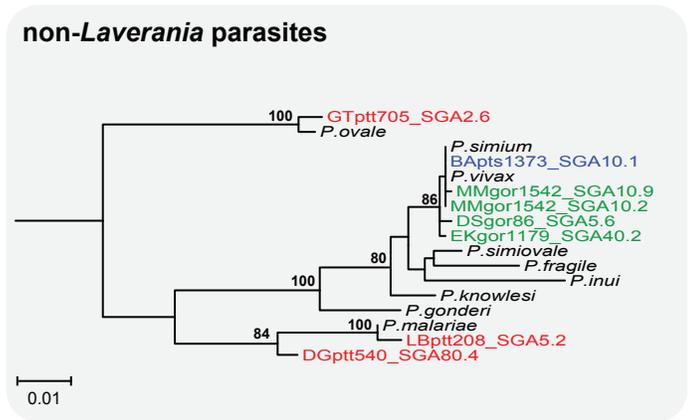
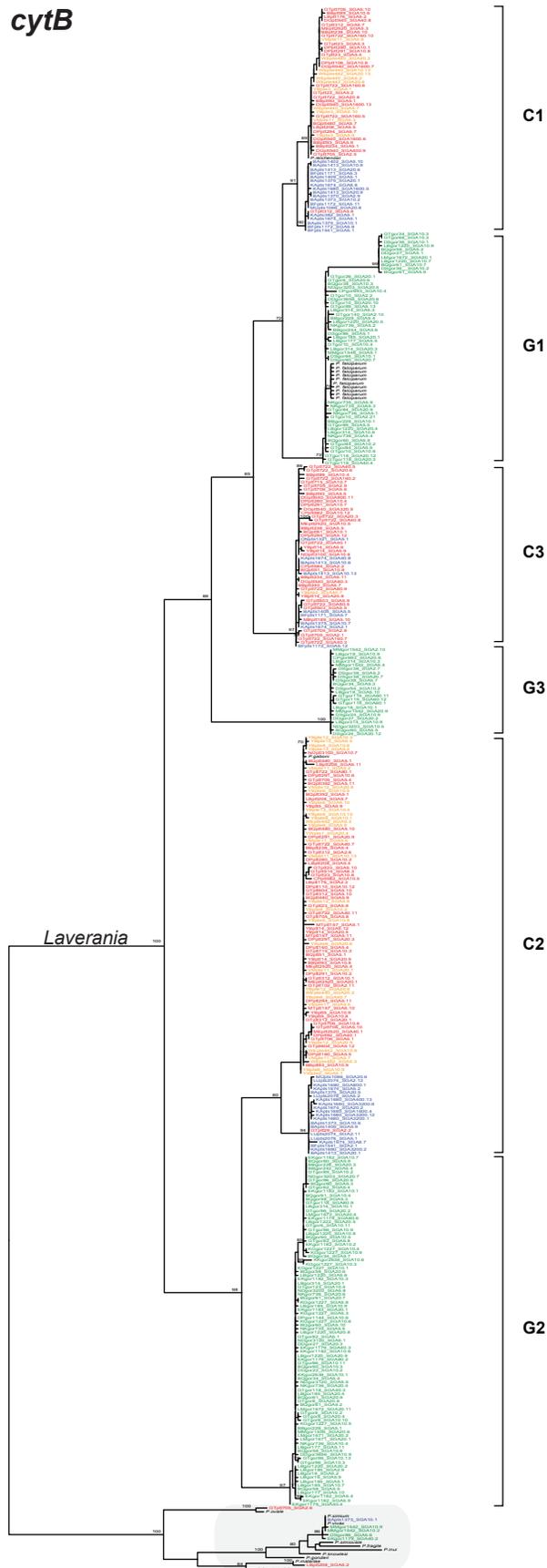
Supplementary Figure 3e

*cytB*



Supplementary Figure 3f

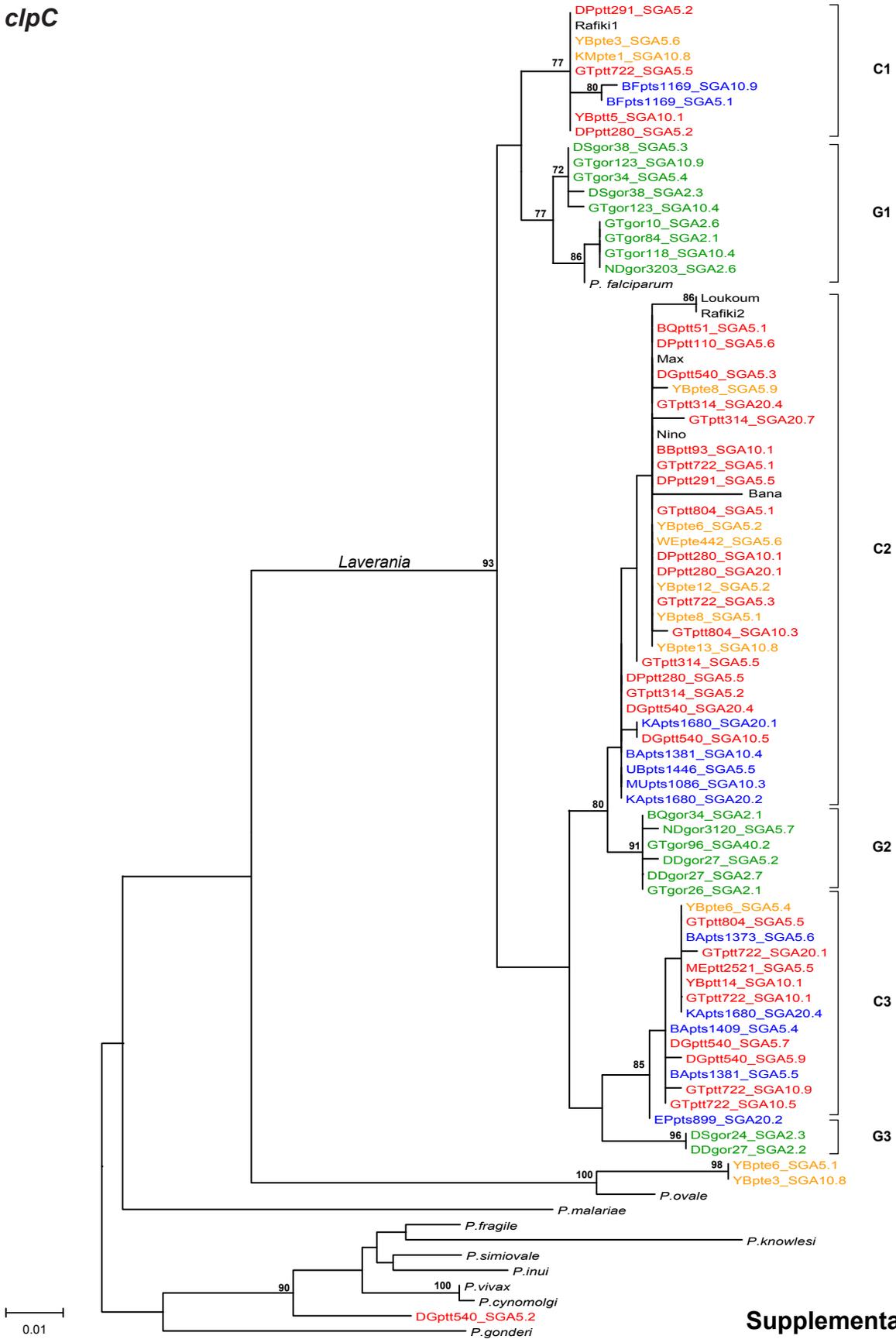
cytB



Supplementary Figure 3g

**Supplementary Figure 3. Evolutionary relationships of ape *Plasmodium* cytochrome B (*cytB*) sequences derived by single genome amplification.** a-g, A total of 697 *Plasmodium cytB* sequences (956 bp) were derived by SGA from the same 118 fecal samples shown in Supplementary Fig. 2 (389 distinct sequences are shown; identical sequences from the same sample were excluded). In each panel, the complete phylogenetic tree is shown on the left, with individual *Laverania* (a-f) and non-*Laverania* (g) clades magnified on the right. Sequences are color-coded, with capital letters indicating the field site (Fig. 1) and lower case letters denoting the species and subspecies origin (ptt: *P. t. troglodytes*, red; pte: *P. t. ellioti*, orange; pts: *P. t. schweinfurthii*, blue; gor: *G. g. gorilla*, green). SGA dilution and well numbers are also indicated (e.g., GTptt705\_SGA5.10 represents an SGA derived sequence amplified from a 1:5 dilution of GTptt705 fecal DNA and identified at position 10 in a plate of multiple PCR reactions). Human and simian *Plasmodium* reference sequences are shown in black (see Supplementary Table 7 for GenBank accession numbers). Diamonds highlight mixed parasite infections in chimpanzee samples GTptt722 (red) and BFpts1541 (blue), and in gorilla sample LBgor314 (green); sequences from the corresponding bulk PCR analysis are shown in Supplementary Fig. 2. The phylogenetic tree was inferred using PhyML<sup>30</sup>; numbers on nodes indicate bootstrap replicates (only values above 70% are shown). The scale bar represents 0.01 substitutions per site.

clpC

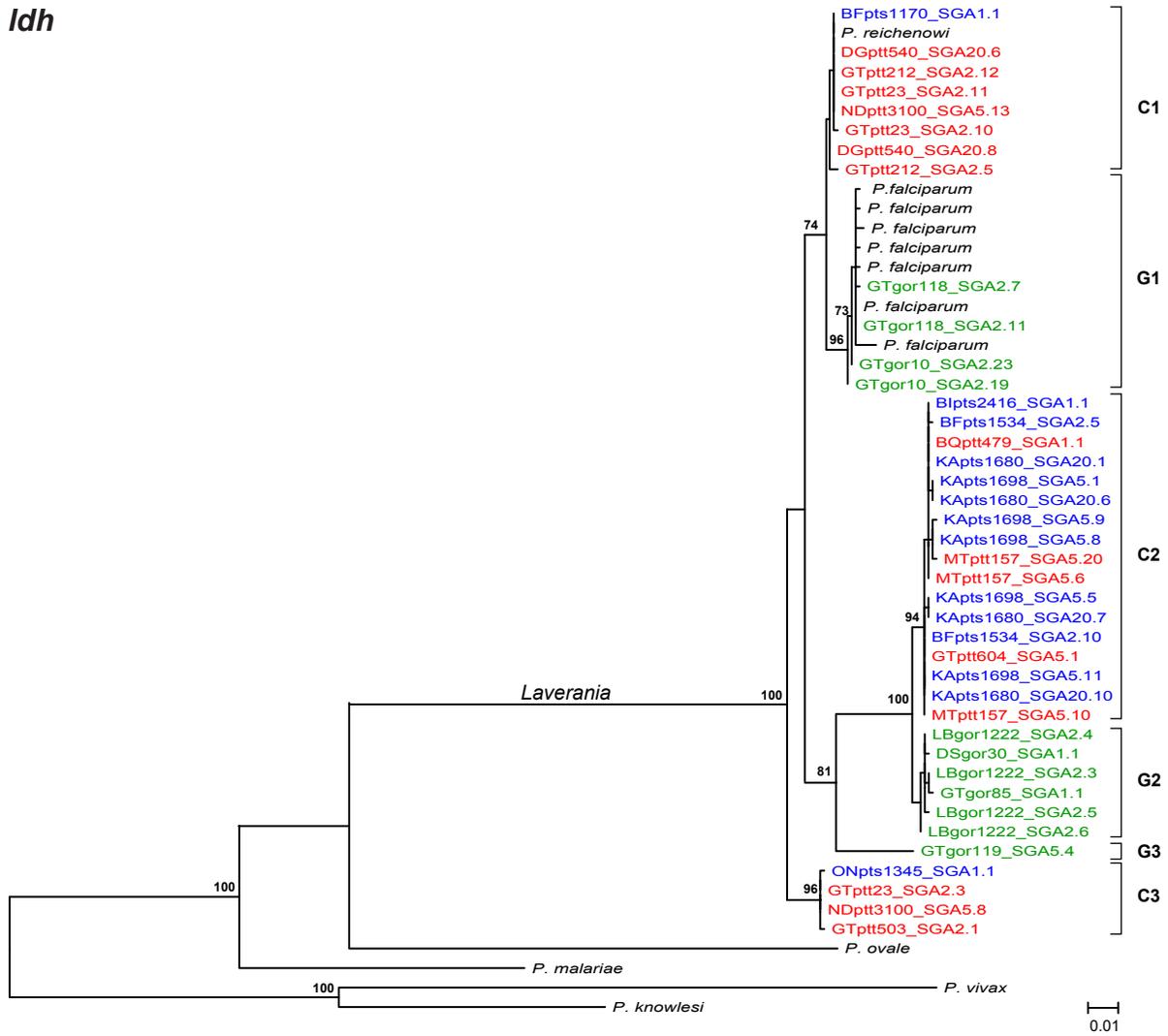


Supplementary Figure 4

**Supplementary Figure 4. Evolutionary relationships of ape *Plasmodium* caseinolytic protease C (*clpC*) sequences derived by single genome amplification.**

72 SGA-derived apicoplast-encoded *clpC* sequences (390 bp) from 40 fecal samples are shown. Newly derived ape *Plasmodium* sequences are labeled and color-coded as in Supplementary Fig. 3. Human and simian reference sequences are shown in black (see Supplementary Table 7 for GenBank accession numbers). Because of a lack of reference sequences in the *clpC* gene, clades C2, C3, G2 and G3 were tentatively assigned based on their relative parasite frequencies as shown in Supplemental Fig. 3 (clades G1 and C1 were identified based on their relationships with human *P. falciparum*). The phylogenetic tree was inferred using PhyML<sup>30</sup>; numbers on nodes indicate bootstrap replicates (only values above 70% are shown). The scale bar represents 0.01 substitutions per site.

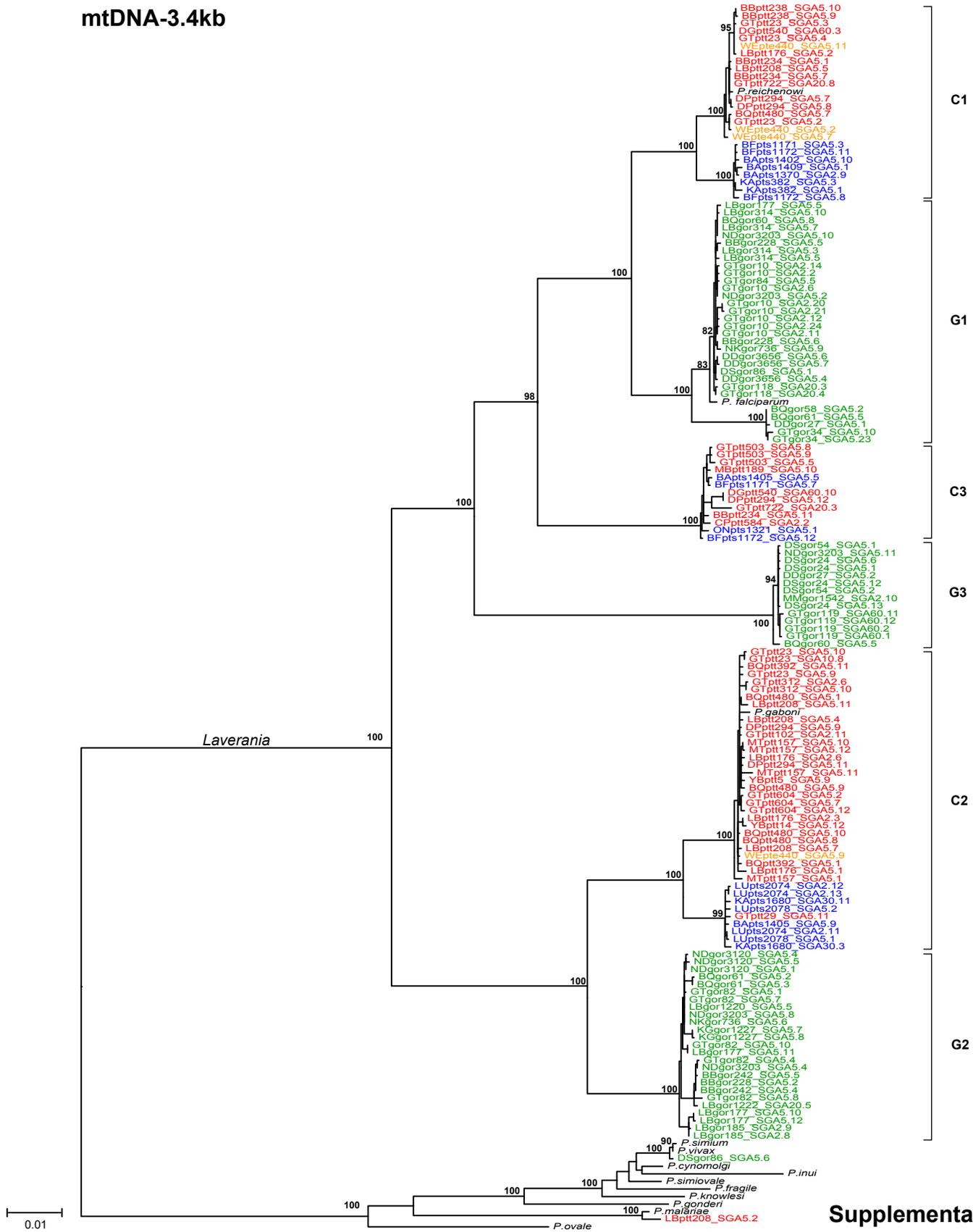
ldh



Supplementary Figure 5

**Supplementary Figure 5. Evolutionary relationships of ape *Plasmodium* lactate dehydrogenase (*ldh*) sequences derived by single genome amplification.** 40 SGA-derived nuclear *ldh* sequences (772 bp) from 20 fecal samples are shown. Newly derived ape *Plasmodium* sequences are labeled and color-coded as in Supplementary Fig. 3. Human and simian reference sequences are shown in black (see Supplementary Table 7 for GenBank accession numbers). Clades C2, C3, G2 and G3 were tentatively designated as in Supplementary Fig. 4. The phylogenetic tree was inferred using PhyML<sup>30</sup>; numbers on nodes indicate bootstrap replicates (only values above 70% are shown). The scale bar represents 0.01 substitutions per site.

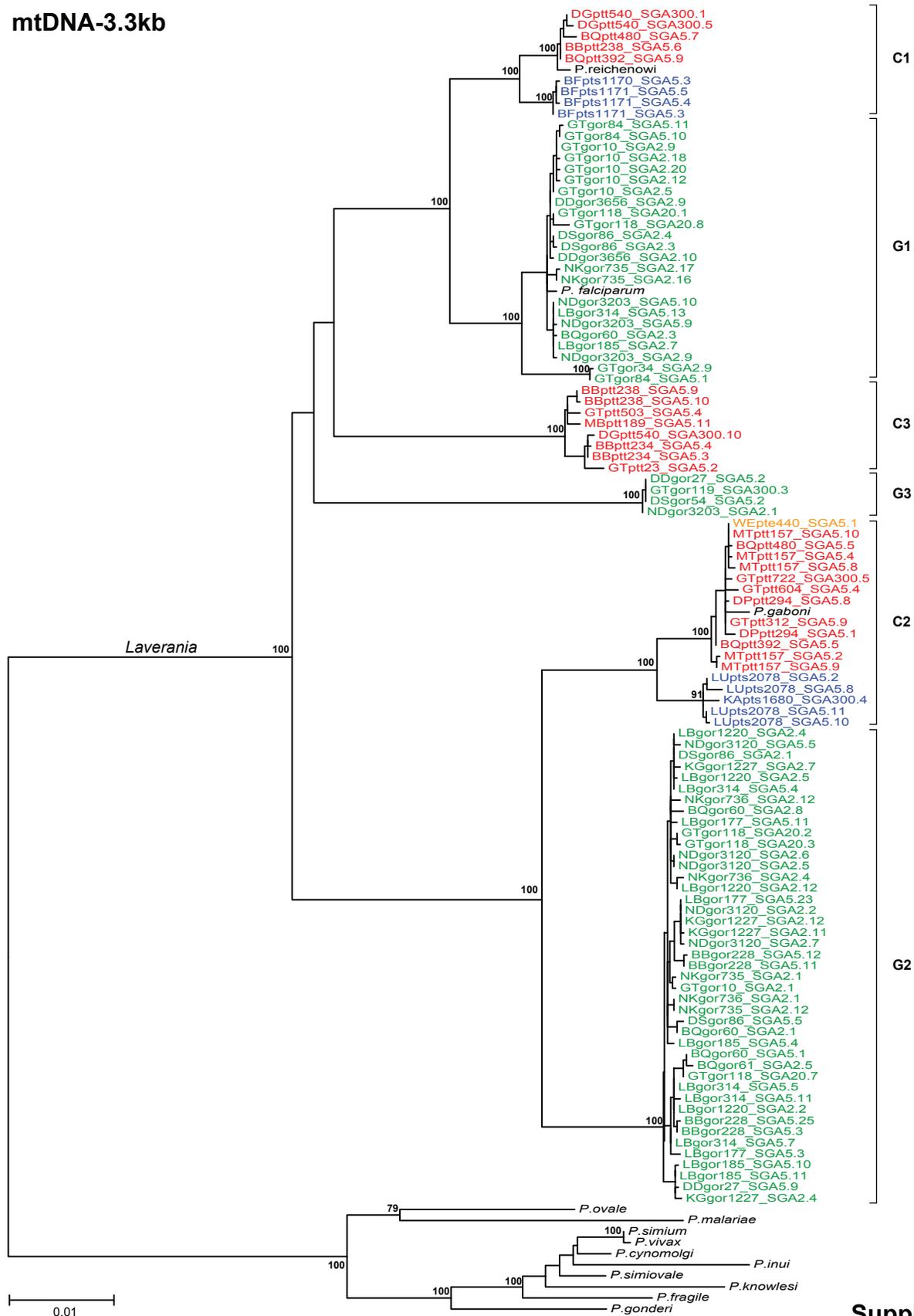
mtDNA-3.4kb



Supplementary Figure 6

**Supplementary Figure 6. Evolutionary relationships of ape *Plasmodium* mitochondrial sequences (3.4 kb fragment) derived by single genome amplification.** 149 SGA-derived mitochondrial half genome sequences (3,361 bp) from 58 ape fecal samples are shown (see Supplementary Fig 1a for position in the mitochondrial genome). Newly derived ape *Plasmodium* sequences are labeled and color-coded as in Supplementary Fig. 3. Human and simian reference sequences are shown in black (see Supplementary Table 7 for GenBank accession numbers). The phylogenetic tree was inferred using PhyML<sup>30</sup>; numbers on nodes indicate bootstrap replicates (only values above 70% are shown). The scale bar represents 0.01 substitutions per site.

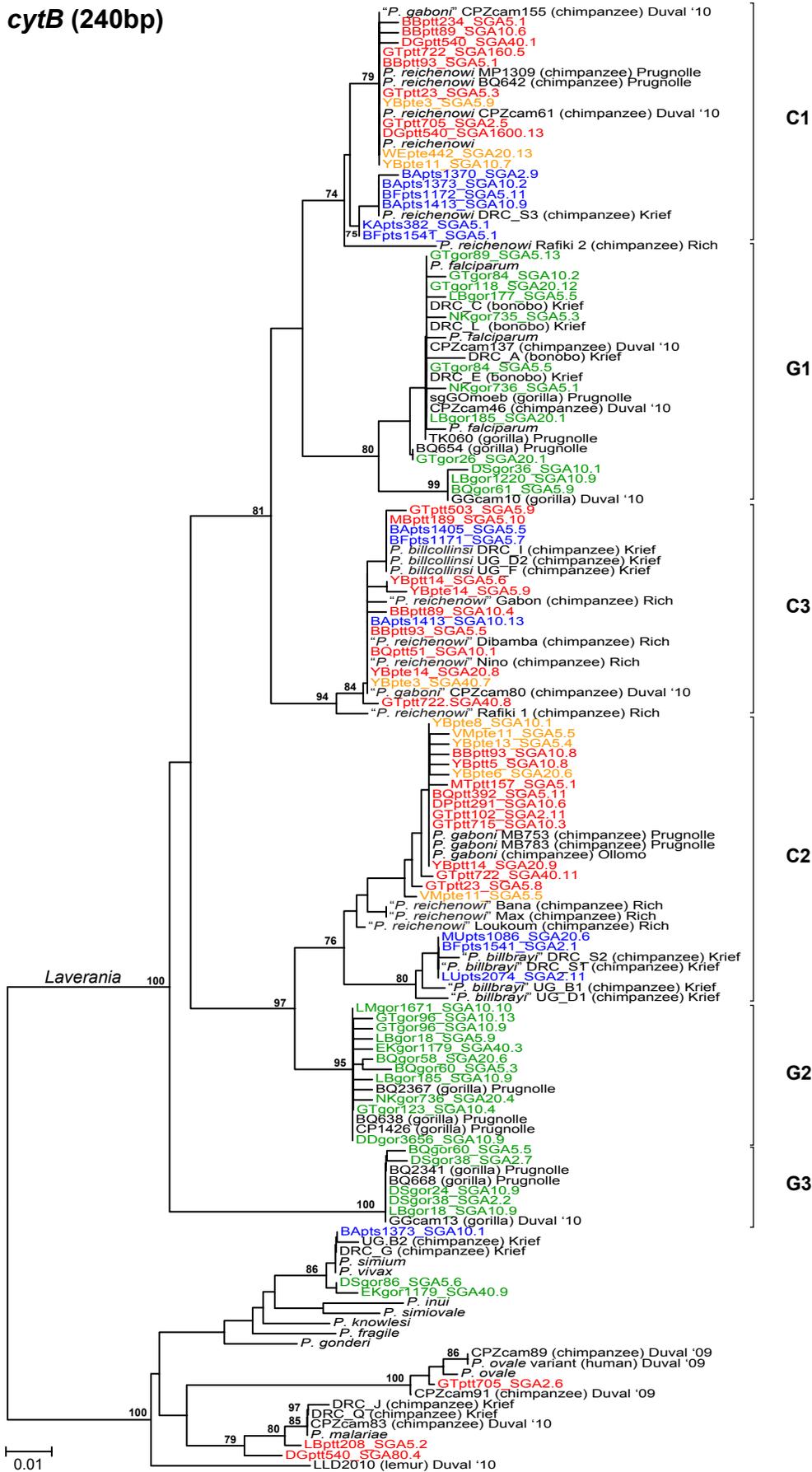
mtDNA-3.3kb



Supplementary Figure 7

**Supplementary Figure 7. Evolutionary relationships of ape *Plasmodium* mitochondrial sequences (3.3 kb fragment) derived by single genome amplification.** 105 SGA-derived mitochondrial half genome sequences (3,277 bp) from 39 ape fecal samples are shown (see Supplementary Fig 1a for position in the mitochondrial genome). Newly derived ape *Plasmodium* sequences are labeled and color-coded as in Supplementary Fig. 3. Human and simian reference sequences are shown in black (see Supplementary Table 7 for GenBank accession numbers). The phylogenetic tree was inferred using PhyML<sup>30</sup>; numbers on nodes indicate bootstrap replicates (only values above 70% are shown). The scale bar represents 0.01 substitutions per site.

cytB (240bp)



Supplementary Figure 8

**Supplementary Figure 8. Position of previously reported ape *Plasmodium* sequences within the *Laverania* subgenus.** Chimpanzee and gorilla *Plasmodium* sequences reported by Ollomo<sup>27</sup>, Duval<sup>12,28</sup>, Rich<sup>9</sup>, Prugnolle<sup>10</sup>, and Krief<sup>11</sup> are shown in relation to 82 SGA derived ape *Plasmodium* sequences in a 240 bp *cytB* region where all sequences overlap. All previously and newly derived sequences fall into six chimpanzee (C1-C3) and gorilla (G1-G3) specific clades, arguing strongly for the existence of six distinct *Plasmodium* species within the *Laverania* subgenus. C1, C2 and C3 have previously been termed *P. reichenowi*, *P. gaboni*, and *P. billcollinsi* on the basis of a limited number of parasite strains<sup>9-11</sup>, while the three species from gorilla had until now not been identified as discrete *Plasmodium* lineages. Formal classification of these lineages must await additional taxonomic evaluation. SGA-derived *Plasmodium* sequences are labeled and color-coded as in Supplementary Fig. 3. Human and simian reference sequences are shown in black (see Supplementary Table 7 for GenBank accession numbers). Note the long branches of some previously reported ape *Plasmodium* sequences, which likely represent bulk PCR artifacts. Quotation marks indicate members of clades that were previously misidentified. The phylogenetic tree was constructed using the neighbor-joining method<sup>37</sup>. Numbers on nodes indicate bootstrap replicates (only values above 70% are shown). The scale bar represents 0.01 substitutions per site.

**Supplementary Table 1. Prevalence of *Plasmodium* infection in wild-living apes throughout central Africa**

Field Sites <sup>a</sup>	Country <sup>b</sup>	Subspecies <sup>c</sup>	Chimpanzee ( <i>Pan</i> )			Gorilla ( <i>Gorilla</i> )				
			Samples tested/positive <sup>d</sup>	Individuals Tested/positive <sup>e</sup>	Plasmodium Prevalence (%) <sup>f</sup>	Subspecies <sup>c</sup>	Samples tested/positive <sup>d</sup>	Individuals tested/positive <sup>e</sup>	Plasmodium Prevalence (%) <sup>f</sup>	
EB	Cameroon	<i>P.t.e.</i>	26/1	--/9	8	(0-32)				
YW	Cameroon	<i>P.t.e.</i>	4/2	--/--	100	(22-100)				
LH	Cameroon	<i>P.t.e.</i>	7/0	--/--	0	(0-63)				
VM	Cameroon	<i>P.t.e.</i>	5/2	--/--	81	(22-100)				
MF	Cameroon	<i>P.t.e.</i>	13/0	--/--	0	(0-39)				
NT <sup>h</sup>	Cameroon	<i>P.t.e.</i>	9/0	--/--	0	(0-53)				
		<i>P.t.t.</i>	2/0	--/--	0	(0-95)				
WE <sup>h</sup>	Cameroon	<i>P.t.e.</i>	24/7	--/--	59	(32-82)				
		<i>P.t.t.</i>	2/0	--/--	0	(0-95)				
YB <sup>h</sup>	Cameroon	<i>P.t.e.</i>	20/5	--/--	50	(22-78)				
		<i>P.t.t.</i>	4/2	--/--	100	(22-100)				
KM <sup>h</sup>	Cameroon	<i>P.t.e.</i>	11/2	--/--	37	(8-81)				
		<i>P.t.t.</i>	1/0	--/--	0	(0-95)				
AL	Cameroon						<i>G.g.g.</i>	9/0	--/--	0 (0-53)
BQ	Cameroon	<i>P.t.t.</i>	67/13	--/--	39	(25-55)	<i>G.g.g.</i>	16/8	--/--	100 (69-100)
BB	Cameroon	<i>P.t.t.</i>	25/8	18/5	49	(29-71)	<i>G.g.g.</i>	7/3	--/--	87 (37-100)
CP	Cameroon	<i>P.t.t.</i>	18/2	--/--	22	(4-55)	<i>G.g.g.</i>	76/2	--/--	5 (1-16)
DD	Cameroon	<i>P.t.t.</i>	4/0	--/--	0	(0-78)	<i>G.g.g.</i>	48/8	--/--	34 (19-54)
DG	Cameroon	<i>P.t.t.</i>	29/5	--/--	35	(15-61)	<i>G.g.g.</i>	25/1	--/--	8 (0-34)
DP	Cameroon	<i>P.t.t.</i>	167/35 <sup>i</sup>	46/13 <sup>i</sup>	50	(37-63)	<i>G.g.g.</i>	16/2	--/--	25 (5-60)
EK	Cameroon	<i>P.t.t.</i>	18/1	15/1	12	(2-36)	<i>G.g.g.</i>	12/3	--/--	50 (15-85)
GB	Cameroon						<i>G.g.g.</i>	18/1	--/--	11 (1-47)
KG	Cameroon						<i>G.g.g.</i>	15/2	--/--	27 (5-66)
KK	Cameroon						<i>G.g.g.</i>	7/1	--/--	29 (2-86)
LB	Cameroon	<i>P.t.t.</i>	13/4	8/3	66	(29-89)	<i>G.g.g.</i>	88/11	--/--	25 (14-37)
LM	Cameroon						<i>G.g.g.</i>	30/10	--/--	67 (46-90)
MB	Cameroon	<i>P.t.t.</i>	25/6	18/6	59	(39-80)	<i>G.g.g.</i>	2/0	--/--	0 (0-95)
MM	Cameroon						<i>G.g.g.</i>	20/3	--/--	30 (10-66)
MT	Cameroon	<i>P.t.t.</i>	56/6	--/--	22	(10-38)				
NK	Cameroon						<i>G.g.g.</i>	25/4	--/--	32 (12-61)
DS	CAR						<i>G.g.g.</i>	85/24 <sup>l</sup>	--/--	57 (43-71)
ME	CAR	<i>P.t.t.</i>	5/2	--/--	81	(22-100)	<i>G.g.g.</i>	21/0	--/--	0 (0-26)
ND	CAR						<i>G.g.g.</i>	17/3	--/--	36 (11-71)
GT	RC	<i>P.t.t.</i>	176/63	105/43	72	(64-79)	<i>G.g.g.</i>	122/34	--/--	56 (44-66)
KE	DRC						<i>G.b.g.</i>	109/0	52/0	0 (0-6)
LU	DRC	<i>P.t.s.</i>	131/10	--/--	15	(7-31)	<i>G.b.g.</i>	4/0	4/0	0 (0-53)
OP	DRC	<i>P.t.s.</i>	10/1	--/--	20	(0-78)	<i>G.b.g.</i>	33/0	15/0	0 (0-18)
AM	DRC	<i>P.t.s.</i>	37/0	--/--	0	(0-28)				
AN	DRC	<i>P.t.s.</i>	15/0	--/--	0	(0-63)				
AZ	DRC	<i>P.t.s.</i>	5/0	--/--	0	(0-95)				
BI	DRC	<i>P.t.s.</i>	65/7	--/--	22	(6-44)				
BA	DRC	<i>P.t.s.</i>	286/61	--/--	43	(33-54)				
BF	DRC	<i>P.t.s.</i>	35/23	--/--	100	(69-100)				
BD	DRC	<i>P.t.s.</i>	15/0	--/--	0	(0-63)				
BL	DRC	<i>P.t.s.</i>	7/0	--/--	0	(0-78)				
EP	DRC	<i>P.t.s.</i>	12/2	--/--	34	(2-86)				
IS	DRC	<i>P.t.s.</i>	4/0	--/--	0	(0-95)				
KA	DRC	<i>P.t.s.</i>	117/32	--/--	55	(38-72)				
KS	DRC	<i>P.t.s.</i>	8/0	--/--	0	(0-78)				
KO	DRC	<i>P.t.s.</i>	43/1	--/--	5	(0-26)				
MU	DRC	<i>P.t.s.</i>	35/15	--/--	87	(53-99)				
ON	DRC	<i>P.t.s.</i>	46/18	--/--	79	(44-92)				
PA	DRC	<i>P.t.s.</i>	41/6	--/--	30	(9-61)				
PO	DRC	<i>P.t.s.</i>	7/0	--/--	0	(0-78)				
UB	DRC	<i>P.t.s.</i>	98/4	--/--	8	(2-25)				
WL	DRC	<i>P.t.s.</i>	22/3	--/--	28	(1-66)				
WK	DRC	<i>P.t.s.</i>	11/0	--/--	0	(0-63)				
WB	DRC	<i>P.t.s.</i>	6/1	--/--	34	(0-95)				
WA	DRC	<i>P.t.s.</i>	40/3	--/--	15	(1-43)				
LK	DRC	<i>P.p.</i>	38/0	18/0	0	(0-15)				
KR	DRC	<i>P.p.</i>	69/0	40/0	0	(0-7)				

<sup>a</sup>Field sites are designated by a two letter code (their location is shown in Fig. 1).

<sup>b</sup>CAR, Central African Republic; RC, Republic of the Congo; DRC, Democratic Republic of the Congo.

<sup>c</sup>*P.t.e.*, *Pan troglodytes ellioti*; *P.t.t.*, *P. t. troglodytes*; *P.t.s.*, *P. t. schweinfurthii*; *P.p.*, *Pan paniscus*; *G.g.g.*, *Gorilla gorilla gorilla*; *G.b.g.*, *Gorilla beringei graueri*.

<sup>d</sup>Number of fecal samples tested/number of fecal samples positive for *Plasmodium* mitochondrial sequences by diagnostic (bulk) PCR; all amplification products were sequenced to confirm *Plasmodium* infection.

<sup>e</sup>For a subset of field sites, the number of individual apes was determined by microsatellite analysis; samples were analyzed at four to eight polymorphic loci; numbers represent minimum estimates since individual genotypes were allowed to differ by up to one allele.

<sup>f</sup>Prevalence of *Plasmodium* infection (%) with brackets indicating 95% confidence intervals (only *Laverania* species were included for analysis); values are based on the proportion of positive samples, except for field sites where the number of tested individuals was known.

<sup>g</sup>--: samples were derived from an unknown number of individuals.

<sup>h</sup>Samples collected at the NT, WE, YB and KM field sites represented members of both *P. t. ellioti* and *P. t. troglodytes* subspecies as determined by host mtDNA analysis<sup>14</sup>.

<sup>i</sup>Only a subset (93 of 167) of samples was subjected to microsatellite analyses.

<sup>l</sup>At the DS field site, fecal samples were collected from both habituated (n=28) and non-habituated (n=57) western gorillas.

**Supplementary Table 2. Assessment of sample quality**

Species <sup>a</sup>	Location	Fecal samples	Microsatellite analysis successful <sup>b</sup>	Microsatellite analysis failed <sup>c</sup>	Proportion of degraded samples	References
Chimpanzee ( <i>P.t.t.</i> )	Cameroon	219	182	37	0.169	ref. 14
Chimpanzee ( <i>P.t.t.</i> )	RC	198	176	22	0.111	this study
Chimpanzee ( <i>P.t.s.</i> )	DRC	302	284	18	0.060	ref. 31
Gorilla ( <i>G.b.g.</i> )	DRC	189	145 <sup>d</sup>	44	0.233	this study
Bonobo ( <i>P.p.</i> )	DRC	119	107	12	0.101	this study
<b>Total</b>		<b>1,027</b>	<b>894</b>	<b>133</b>	<b>0.130</b>	

<sup>a</sup>*P.t.t.*, *Pan troglodytes troglodytes*; *P.t.s.*, *Pan troglodytes schweinfurthii*; *G.b.g.*, *Gorilla beringei graueri*; *P.p.*, *Pan paniscus*.

<sup>b</sup>Samples were analyzed at four to eight polymorphic microsatellite loci to identify the number of individuals; individual genotypes were allowed to differ by up to one allele.

<sup>c</sup>Amplification failed at multiple microsatellite loci due to sample degradation.

<sup>d</sup>At the LU field site, one sample failed microsatellite analysis, but could be identified as representing a unique individual based on its mitochondrial haplotype.

**Supplementary Table 3. Estimates of redundant sampling at different field sites**

Species <sup>a</sup>	Field sites <sup>b</sup>	Fecal samples	IDs <sup>c</sup>	Over-sampling	References
Chimpanzee ( <i>P.t.t.</i> )	EK, LB, BB, MB, DP	182	106	1.72	ref. 14
Chimpanzee ( <i>P.t.t.</i> )	DP, MB, LB, BM, SL	38	17	2.24	ref. 16
Chimpanzee ( <i>P.t.t.</i> )	CP	16	5	3.20	ref. 15
Chimpanzee ( <i>P.t.t.</i> )	GT	176	105	1.68	this study
<b>Chimpanzee (<i>P.t.t.</i>)</b>	<b>n=9</b>	<b>412</b>	<b>233</b>	<b>1.77</b>	
Western Gorilla ( <i>G.g.g.</i> )	CP	112	61	1.83	ref. 15
Western Gorilla ( <i>G.g.g.</i> )	DJ	6	3	2.00	ref. 15
<b>Western Gorilla (<i>G.g.g.</i>)</b>	<b>n=2</b>	<b>118</b>	<b>64</b>	<b>1.84</b>	
Chimpanzee ( <i>P.t.s.</i> )	AM, BA, BF, BL	71	12	5.92	ref. 31
Chimpanzee ( <i>P.t.s.</i> )	EP, KA, KS	57	27	2.11	ref. 31
Chimpanzee ( <i>P.t.s.</i> )	LU, MU, OP, PA	98	21	4.67	ref. 31
Chimpanzee ( <i>P.t.s.</i> )	WA, WB, WL, UB	58	16	3.63	ref. 31
<b>Chimpanzee (<i>P.t.s.</i>)</b>	<b>n=16</b>	<b>284</b>	<b>76</b>	<b>3.74</b>	
Eastern Gorilla ( <i>G.b.g.</i> )	KE	109	52	2.10	this study
Eastern Gorilla ( <i>G.b.g.</i> )	LU	4	4	1.00	this study
Eastern Gorilla ( <i>G.b.g.</i> )	OP	33	15	2.20	this study
<b>Eastern Gorilla (<i>G.b.g.</i>)</b>	<b>n=3</b>	<b>146</b>	<b>71</b>	<b>2.01</b>	
Bonobo ( <i>P.p.</i> )	LK	38	18	2.10	this study
Bonobo ( <i>P.p.</i> )	KR	69	40	1.73	this study
<b>Bonobo (<i>P.p.</i>)</b>	<b>n=2</b>	<b>107</b>	<b>58</b>	<b>1.84</b>	

<sup>a</sup>*P.t.t.*, *Pan troglodytes troglodytes*; *P.t.s.*, *Pan troglodytes schweinfurthii*; *G.g.g.*, *Gorilla gorilla gorilla*; *G.b.g.*, *Gorilla beringei graueri*; *P.p.*, *Pan paniscus*.

<sup>b</sup>The location of these field sites is shown in Fig. 1.

<sup>c</sup>The number of sampled individuals (IDs) was identified by microsatellite analysis; samples were analyzed at four to eight polymorphic loci; numbers represent minimum estimates since individual genotypes were allowed to differ by up to one allele.

**Supplementary Table 4. Sensitivity of fecal *Plasmodium* detection**

Location <sup>b</sup>	Number of Apes tested <sup>c</sup>	Diagnostic PCR <sup>a</sup>		
		Number of positive samples	Number of samples tested	Sensitivity (95% CI) <sup>d</sup>
Cameroon	15	20	39	51% (37%-65%)
RC	7	13	19	68% (47%-85%)
DRC	10	33	58	57% (45%-68%)
<b>Total</b>	<b>32</b>	<b>66</b>	<b>116</b>	<b>57% (49%-65%)</b>

<sup>a</sup>*Plasmodium* infection was diagnosed by PCR amplification of a 956-bp mitochondrial DNA (*cytB*) fragment from fecal DNA.

<sup>b</sup>Fecal samples were collected at multiple field sites in Cameroon, the Republic of Congo (RC) and the Democratic Republic of the Congo (DRC).

<sup>c</sup>For some field sites, the number of sampled individuals was identified by microsatellite analyses (Supplementary Table 1); apes were diagnosed as *Plasmodium* infected if at least one fecal sample was positive for *Plasmodium* mtDNA.

<sup>d</sup>The sensitivity of fecal *Plasmodium* detection was calculated by determining the proportion of PCR positive fecal samples (with 95% confidence intervals [CI]) from apes who were sampled on more than one occasion (see Supplementary Methods for details). Because of the unknown duration of naturally occurring *Plasmodium* infections, only samples collected on the same day were included in the analysis. Note that the estimated sensitivities overestimate the real test sensitivities, since infected apes, who yielded only negative samples, are not accounted for. Moreover, the estimates do not address the extent to which blood infected apes shed *Plasmodium* parasites into their feces. Thus, the prevalence rates in Table 1 and Supplementary Table 1 represent only minimum estimates of the true *Plasmodium* infection rates in wild apes.

Supplementary Table 5. Number of *Plasmodium* species in ape fecal samples

No	Sample	<i>cytB</i>			<i>clpC</i>			<i>ldh</i>			mtDNA-3.4kb			mtDNA-3.3kb		
		<i>cytB</i> seqs <sup>a</sup>	<i>cytB</i> haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	<i>clpC</i> seqs <sup>a</sup>	<i>clpC</i> haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	<i>ldh</i> seqs <sup>a</sup>	<i>ldh</i> haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	3.4kb seqs <sup>a</sup>	3.4kb haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	3.3Kb seqs <sup>a</sup>	3.3kb haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>
1	BBptt89	2	2	C1(1) C3(1)												
2	BBptt93	5	5	C1(2) C2(2) C3(1)	1	1	C2(1)									
3	BBptt234	4	2	C1(1) C3(1)							4	3	C1(2) C3(1)	2	2	C3(2)
4	BBptt238	4	3	C1(1) C2(1) C3(1)							2	2	C1(2)	3	3	C1(1) C3(2)
5	BBptt240	1	1	C3(1)												
6	BQptt51	4	3	C2(1) C3(2)	1	1	C2(1)									
7	BQptt392	2	2	C2(2)							2	2	C2(2)	4	3	C1(1) C2(2)
8	BQptt479							1	1	C2(1)						
9	BQptt480	6	4	C1(1) C2(3)							6	5	C1(1) C2(4)	3	2	C1(1) C2(1)
10	CPptt582	3	2	C2(1) C3(1)												
11	CPptt584	1	1	C3(1)							1	1	C3(1)			
12	DGptt540	21	9	C1(5) C3(3) unk(1)	8	6	C2(3) C3(2) unk(1)	2	2	C1(2)	3	2	C1(1) C3(1)	3	3	C1(2) C3(1)
13	DPptt92	1	1	C2(1)												
14	DPptt106	1	1	C1(1)												
15	DPptt110	1	1	C2(1)	3	1	C2(1)									
16	DPptt160	2	2	C2(2)												
17	DPptt280	3	3	C1(1) C2(1) C3(1)	8	4	C1(1) C2(3)									
18	DPptt291	10	6	C1(1) C2(4) C3(1)	4	2	C1(1) C2(1)									
19	DPptt294	5	3	C1(1) C2(1) C3(1)							5	5	C1(2) C2(2) C3(1)	3	2	C2(2)
20	GTptt23	6	6	C1(3) C2(3)				4	3	C1(2) C3(1)	6	6	C1(3) C2(3)	1	1	C3(1)
21	GTptt29	3	1	C2(1)							3	1	C2(1)			
22	GTptt102	1	1	C2(1)							1	1	C2(1)			
23	GTptt212							2	2	C1(2)						
24	GTptt312	10	6	C1(2) C2(4)							2	2	C2(2)	1	1	C2(1)
25	GTptt314				4	4	C2(4)									
26	GTptt503	3	2	C3(2)				1	1	C3(1)	3	3	C3(3)	2	1	C3(1)
27	GTptt514	3	1	C2(1)												
28	GTptt604	6	2	C2(2)				1	1	C2(1)	6	3	C2(3)	1	1	C2(1)
29	GTptt705	9	8	C1(2) C2(2) C3(3) ovale(1)												
30	GTptt706	17	4	C2(3) C3(1)												
31	GTptt715	2	2	C2(1) C3(1)												
32	GTptt722	40	17	C1(4) C2(3) C3(10)	14	7	C1(1) C2(2) C3(4)				2	2	C1(1) C3(1)	1	1	C2(1)
33	GTptt804				7	3	C2(2) C3(1)									
34	LBptt176	4	2	C1(1) C2(1)							4	4	C1(1) C2(3)			



No	Sample	cytB			clpC			ldh			mtDNA-3.4kb			mtDNA-3.3kb		
		cytB seqs <sup>a</sup>	cytB haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	clpC seqs <sup>a</sup>	clpC haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	ldh seqs <sup>a</sup>	ldh haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	3.4kb seqs <sup>a</sup>	3.4kb haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	3.3Kb seqs <sup>a</sup>	3.3kb haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>
77	YBpte12	5	4	C2(4)	2	1	C2(1)									
78	YBpte13	3	3	C2(3)	2	1	C2(1)									
79	YWpte1	2	1	C2(1)												
80	YWpte2	1	1	C2(1)												
1	BBgor228	12	4	G1(2) G2(2)							3	3	G1(2) G2(1)	6	4	G2(4)
2	BBgor242	2	1	G2(1)							2	2	G2(2)			
3	BBgor244	1	1	G1(1)												
4	BQgor34	4	4	G1(1) G2(2) G3(1)	1	1	G2(1)									
5	BQgor58	5	5	G1(1) G2(4)							1	1	G1(1)			
6	BQgor60	11	7	G1(1) G2(5) G3(1)							3	2	G1(1) G3(1)	4	4	G1(1) G2(3)
7	BQgor61	12	6	G1(2) G2(4)							3	3	G1(1) G2(2)	1	1	G2(1)
8	CPgor693	2	2	G1(1) G3(1)												
9	DDgor22	1	1	G2(1)												
10	DDgor27	6	3	G1(1) G2(1) G3(1)	3	3	G2(2) G3(1)				4	2	G1(1) G3(1)	3	2	G2(1) G3(1)
11	DDgor3656	5	2	G1(1) G2(1)							3	3	G1(3)	2	2	G1(2)
12	DPgor1144	2	1	G2(1)												
13	DSgor24	10	2	G3(2)	2	1	G3(1)				5	4	G3(4)			
14	DSgor30							1	1	G2(1)						
15	DSgor36	4	2	G1(2)												
16	DSgor38	6	4	G3(4)	2	2	G1(2)									
17	DSgor54	3	1	G3(1)							2	2	G3(2)	2	1	G3(1)
18	DSgor60	1	1	G1(1)												
19	DSgor64	2	1	G1(1)												
20	DSgor86	2	2	G1(1) vivax(1)							2	2	G1(1) vivax(1)	5	4	G1(2) G2(2)
21	EKgor1179	17	12	G2(4) vivax(8)												
22	EKgor1182	8	7	G2(7)												
23	EKgor1183	1	1	G2(1)												
24	GTgor6	2	2	G1(1) G2(1)												
25	GTgor8	7	4	G2(4)												
26	GTgor10	15	5	G1(5)	4	1	G1(1)	2	2	G1(2)	8	8	G1(8)	11	6	G1(5) G2(1)
27	GTgor26	1	1	G1(1)	1	1	G2(1)									
28	GTgor34	4	1	G1(1)	1	1	G1(1)				2	2	G1(2)	1	1	G1(1)
29	GTgor68	1	1	G1(1)												
30	GTgor82	5	3	G2(3)							5	5	G2(5)			
31	GTgor84	8	3	G1(3)	7	1	G1(1)				1	1	G1(1)	3	3	G1(3)
32	GTgor85							1	1	G2(1)						
33	GTgor89	3	3	G1(2) G2(1)												
34	GTgor96	10	6	G2(6)	1	1	G2(1)									
35	GTgor118	6	5	G1(3) G2(2)	1	1	G1(1)	2	2	G1(2)	3	2	G1(2)	5	5	G1(2) G2(3)
36	GTgor119	31	3	G3(3)				2	1	G3(1)	7	4	G3(4)	4	1	G3(1)
37	GTgor123	5	1	G2(1)	2	2	G1(2)									
38	GTgor140	1	1	G1(1)												
39	KGgor1227	12	8	G2(8)							2	2	G2(2)	4	4	G2(4)
40	KKgor2638	2	2	G2(2)												
41	LBgor18	6	5	G2(2) G3(3)												
42	LBgor177	4	3	G1(1) G2(2)							4	4	G1(1), G2(3)	3	3	G2(3)
43	LBgor185	13	6	G1(1) G2(5)							2	2	G2(2)	4	4	G1(1) G2(3)

No	Sample	<i>cytB</i>			<i>clpC</i>			<i>ldh</i>			mtDNA-3.4kb			mtDNA-3.3kb		
		<i>cytB</i> seqs <sup>a</sup>	<i>cytB</i> haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	<i>clpC</i> seqs <sup>a</sup>	<i>clpC</i> haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	<i>ldh</i> seqs <sup>a</sup>	<i>ldh</i> haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	3.4kb seqs <sup>a</sup>	3.4kb haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>	3.3Kb seqs <sup>a</sup>	3.3kb haplo-types <sup>b</sup>	<i>P. spp.</i> <sup>c</sup>
44	LBgor314	11	7	G1(3) G2(2) G3(2)							4	4	G1(4)	7	5	G1(1) G2(4)
45	LBgor1220	12	9	G1(4) G2(5)							1	1	G2(1)	4	4	G2(4)
46	LBgor1222	1	1	G2(1)				4	4	G2(4)	1	1	G2(1)			
47	LMgor1671	12	2	G2(2)												
48	LMgor1672	6	3	G1(1) G2(2)												
49	MMgor1536	1	1	G2(1)												
50	MMgor1542	6	5	G3(3) vivax(2)							1	1	G3(1)			
51	MMgor1546	2	1	G1(1)												
52	NDgor3120	3	2	G2(2)	1	1	G2(1)				3	3	G2(3)	5	5	G2(5)
53	NDgor3203	12	4	G1(1) G2(2) G3(1)	1	1	G1(1)				5	5	G1(2) G2(2) G3(1)	5	4	G1(3) G3(1)
54	NKgor0735	3	3	G1(2) G2(1)										4	4	G1(2) G2(2)
55	NKgor0736	12	6	G1(3) G2(3)							2	2	G1(1) G2(1)	3	3	G2(3)
<b>135</b>	<b>Total</b>	<b>697</b>	<b>396</b>		<b>126</b>	<b>72</b>		<b>46</b>	<b>40</b>		<b>165</b>	<b>149</b>		<b>127</b>	<b>106</b>	

<sup>a</sup>Number of SGA amplicons sequenced.

<sup>b</sup>Number of unique SGA haplotypes.

<sup>c</sup>Number of *Plasmodium* species (*P. spp.*) as defined in Supplementary Figs. 3-8, with the number of unique SGA sequences listed in parentheses; the species origin of *cytB* and *clpC* sequences in sample DGptt540 remains unknown (unk).

**Supplementary Table 6. GenBank accession numbers of SGA-derived *Plasmodium* sequences**

No	Sample	cytB	Accession No.	mtDNA-3.4kb SGA	Accession No.	mtDNA-3.3kb	Accession No.	ldh	Accession No.	cipC	Accession No.	
1	BBptt89	BBptt89_SGA10.4 BBptt89_SGA10.6	HM234977 HM234978									
2	BBptt93	BBptt93_SGA10.8 BBptt93_SGA10.9 BBptt93_SGA5.1 BBptt93_SGA5.5 BBptt93_SGA5.9	HM234979 =BQptt392_SGA5.1(3.4Kb) HM234980 HM234981 =BQptt480_SGA5.7(3.4Kb)							BBptt93_SGA10.1	HM235145	
3	BBptt234	BBptt234_SGA5.1 (3.4kb cytB) BBptt234_SGA5.7 (3.4kb cytB) BBptt234_SGA5.12 (3.4kb cytB) BBptt234_SGA5.11 (3.4kb cytB)	=BBptt234_SGA5.1(3.4Kb) =GTPtt722_SGA20.8(3.4Kb) =GTPtt722_SGA20.8(3.4Kb) =BBptt234_SGA5.11(3.4Kb)	BBptt234_SGA5.1 BBptt234_SGA5.7 BBptt234_SGA5.12 BBptt234_SGA5.11	HM235350 =GTPtt722_SGA20.8 =GTPtt722_SGA20.8 HM235351	BBptt234_SGA5.3 BBptt234_SGA5.4	HM235175 HM235176					
4	BBptt238	BBptt238_SGA5.2 BBptt238_SGA5.4 BBptt238_SGA5.9 (3.4kb cytB) BBptt238_SGA5.10 (3.4kb cytB)	=DQptt540_SGA60.10(3.4Kb) =BQptt392_SGA5.1(3.4Kb) =BBptt238_SGA5.9(3.4Kb) =BBptt238_SGA5.10(3.4Kb)	BBptt238_SGA5.9 BBptt238_SGA5.10	HM235299 HM235300	BBptt238_SGA5.6 BBptt238_SGA5.9 BBptt238_SGA5.10	HM235178 HM235179 HM235177					
5	BBptt240	BBptt240_SGA5.7	=BFpts1172_SGA5.12(3.4Kb)									
6	BQptt51	BQptt51_SGA10.1 BQptt51_SGA10.8 BQptt51_SGA5.1 BQptt51_SGA5.3	HM234983 =CPptt584_SGA2.2(3.4Kb) =BQptt392_SGA5.1(3.4Kb) =BQptt392_SGA5.1(3.4Kb)							BQptt51_SGA5.1	=BBptt93_SGA10.1	
7	BQptt392	BBptt392_SGA5.1 (3.4kb cytB) BBptt392_SGA5.11 (3.4kb cytB)	=BQptt392_SGA5.1(3.4Kb) =BBptt392_SGA5.1(3.4Kb) =BBptt392_SGA5.11(3.4Kb)	BBptt392_SGA5.1 BBptt392_SGA5.11	HM235352 HM235353	BBptt392_SGA5.5 BBptt392_SGA5.6 BBptt392_SGA5.9 BBptt392_SGA5.11	HM235169 HM235190 =BBptt238_SGA5.6 =BBptt392_SGA5.11					
8	BQptt479							BQptt479_SGA1.1	=MTptt157_SGA5.6			
9	BQptt480	BQptt480_SGA5.7 (3.4kb cytB) BQptt480_SGA5.11 (3.4kb cytB) BQptt480_SGA5.1 (3.4kb cytB) BQptt480_SGA5.8 (3.4kb cytB) BQptt480_SGA5.9 (3.4kb cytB) BQptt480_SGA5.10 (3.4kb cytB)	=BQptt480_SGA5.7(3.4Kb) =BQptt480_SGA5.7(3.4Kb) =BQptt480_SGA5.1(3.4Kb) =BQptt480_SGA5.8(3.4Kb) =BQptt480_SGA5.9(3.4Kb) =BQptt480_SGA5.10(3.4Kb)	BQptt480_SGA5.7 BQptt480_SGA5.11 BQptt480_SGA5.1 BQptt480_SGA5.8 BQptt480_SGA5.9 BQptt480_SGA5.10	HM235355 =BQptt480_SGA5.7 HM235354 HM235356 HM235358 HM235357	BQptt480_SGA5.5 BQptt480_SGA5.7 BQptt480_SGA5.10	HM235191 HM235192 =BQptt480_SGA5.7					
10	CPptt582	CPptt582_SGA10.5 CPptt582_SGA10.7 CPptt582_SGA10.12	HM234989 =DQptt540_SGA60.10(3.4Kb) =DQptt540_SGA60.10(3.4Kb)									
11	CPptt584	CPptt584_SGA2.2 (3.4kb cytB)	=CPptt584_SGA2.2(3.4Kb)	CPptt584_SGA2.2	HM235293							
12	DGptt540	DGptt540_SGA10.2 DGptt540_SGA1600.13 DGptt540_SGA1600.6 DGptt540_SGA1600.7 DGptt540_SGA320.5 DGptt540_SGA20.4 DGptt540_SGA40.1 DGptt540_SGA40.8 DGptt540_SGA400.9 DGptt540_SGA400.3 DGptt540_SGA800.4 DGptt540_SGA80.5 DGptt540_SGA80.8 DGptt540_SGA800.1 DGptt540_SGA800.2 DGptt540_SGA800.9 DGptt540_SGA800.11 DGptt540_SGA60.3 (3.4kb cytB) DGptt540_SGA60.12 (3.4kb cytB) DGptt540_SGA60.10 (3.4kb cytB)	=BBptt238_SGA5.10(3.4Kb) =DQptt540_SGA60.10(3.4Kb) HM234992 =BQptt480_SGA5.7(3.4Kb) =BBptt238_SGA5.10(3.4Kb) HM234993 =BQptt480_SGA5.7(3.4Kb) =DQptt540_SGA800.2 =BBptt234_SGA5.11(3.4Kb) HM234994 =BQptt480_SGA5.7(3.4Kb) =BBptt238_SGA5.10(3.4Kb) =BBptt238_SGA5.10(3.4Kb) HM234995 =DQptt540_SGA60.10(3.4Kb) =DQptt540_SGA60.10(3.4Kb) =DQptt540_SGA60.3(3.4Kb) =DQptt540_SGA60.3(3.4Kb) =DQptt540_SGA60.10(3.4Kb)	DGptt540_SGA60.3 DGptt540_SGA60.12 DGptt540_SGA60.10	HM235359 =DQptt540_SGA60.3 HM235360	DGptt540_SGA300.1 DGptt540_SGA300.5 DGptt540_SGA300.10	HM235196 HM235198 HM235197	DGptt540_SGA20.6 DGptt540_SGA20.8	HM235135 HM235136	DGptt540_SGA20.4 DGptt540_SGA10.3 DGptt540_SGA10.5 DGptt540_SGA5.2 DGptt540_SGA5.3 DGptt540_SGA5.5 DGptt540_SGA5.7 DGptt540_SGA5.9	=UBpts1446_SGA5.5 =BBptt93_SGA10.1 =KApst160_SGA20.1 HM235150 =BBptt93_SGA10.1 =BBptt93_SGA10.1 =BApst1381_SGA5.5 HM235151	
13	DPptt92	DPptt92_SGA40.1	=GTPtt706_SGA10.6									
14	DPptt106	DPptt106_SGA10.8	=BBptt238_SGA5.10(3.4Kb)									
15	DPptt110	DPptt110_SGA10.12	=BQptt392_SGA5.1(3.4Kb)							DPptt110_SGA10.2 DPptt110_SGA10.3 DPptt110_SGA5.6	=BBptt93_SGA10.1 =BBptt93_SGA10.1 =BBptt93_SGA10.1	
16	DPptt160	DPptt160_SGA5.4 DPptt160_SGA5.5	=BQptt392_SGA5.1(3.4Kb) HM235112									
17	DPptt280	DPptt280_SGA10.1 DPptt280_SGA10.2 DPptt280_SGA10.4	HM235107 =BQptt392_SGA5.1(3.4Kb) =DQptt540_SGA60.10(3.4Kb)							DPptt280_SGA20.1	HM235152	
18	DPptt291	DPptt291_SGA10.2 DPptt291_SGA10.6 DPptt291_SGA10.7 DPptt291_SGA10.8 DPptt291_SGA10.9 DPptt291_SGA20.3 DPptt291_SGA20.5 DPptt291_SGA20.6 DPptt291_SGA20.7 DPptt291_SGA20.9	=BQptt392_SGA5.1(3.4Kb) =DPptt291_SGA20.5 =DQptt540_SGA60.10(3.4Kb) =DPptt280_SGA10.1 =BQptt480_SGA5.8(3.4Kb) HM234996 HM234997 =BQptt480_SGA5.8(3.4Kb) =BQptt480_SGA5.8(3.4Kb) HM237301							DPptt291_SGA10.1 DPptt291_SGA5.5 DPptt291_SGA10.2 DPptt291_SGA5.2 DPptt291_SGA5.5 =BBptt93_SGA10.1		
19	DPptt294	DPptt294_SGA5.7 (3.4kb cytB) DPptt294_SGA5.8 (3.4kb cytB) DPptt294_SGA5.12 (3.4kb cytB) DPptt294_SGA5.9 (3.4kb cytB) DPptt294_SGA5.11 (3.4kb cytB)	=DPptt294_SGA5.7(3.4Kb) =DPptt294_SGA5.8(3.4Kb) =DQptt540_SGA60.10(3.4Kb) =DPptt294_SGA5.9(3.4Kb) =DPptt294_SGA5.11(3.4Kb)	DPptt294_SGA5.7 DPptt294_SGA5.8 DPptt294_SGA5.12 DPptt294_SGA5.9 DPptt294_SGA5.11	HM235321 HM235322 =DQptt540_SGA60.10 HM235323 HM235324	DPptt294_SGA5.1 DPptt294_SGA5.8 DPptt294_SGA5.10	HM235199 HM235200 =DPptt294_SGA5.8					
20	GTptt23	GTptt23_SGA5.2 (3.4kb cytB) GTptt23_SGA5.3 (3.4kb cytB) GTptt23_SGA5.4 (3.4kb cytB) GTptt23_SGA5.9 (3.4kb cytB) GTptt23_SGA5.10 (3.4kb cytB) GTptt23_SGA10.8 (3.4kb cytB)	=GTPtt23_SGA5.2(3.4Kb) =GTPtt23_SGA5.3(3.4Kb) =DQptt540_SGA60.3(3.4Kb) =GTPtt23_SGA5.9(3.4Kb) =GTPtt23_SGA5.10(3.4Kb) =GTPtt23_SGA10.8(3.4Kb)	GTptt23_SGA5.2 GTptt23_SGA5.3 GTptt23_SGA5.4 GTptt23_SGA5.9 GTptt23_SGA5.10 GTptt23_SGA10.8	HM235327 HM235328 =DQptt540_SGA60.3 HM235331 HM235330 HM235329	GTptt23_SGA5.1 GTptt23_SGA2.11 GTptt23_SGA2.3 GTptt23_SGA2.10	=DQptt540_SGA20.6 =DQptt540_SGA20.6 =NDptt3100_SGA5.8 HM235126					
21	GTptt29	GTptt29_SGA2.2 (3.4kb cytB) GTptt29_SGA2.8 (3.4kb cytB) GTptt29_SGA5.11 (3.4kb cytB)	=GTPtt29_SGA5.11(3.4Kb) =GTPtt29_SGA5.11(3.4Kb) =GTPtt29_SGA5.11(3.4Kb)	GTptt29_SGA2.2 GTptt29_SGA2.8 GTptt29_SGA5.11	=GTPtt29_SGA5.11 =GTPtt29_SGA5.11 HM235343							
22	GTptt102	GTptt102_SGA5.11 (3.4kb cytB)	=GTPtt102_SGA2.11(3.4Kb)									
23	GTptt212							GTptt212_SGA2.5 GTptt212_SGA2.12	HM235118 =DQptt540_SGA20.6			
24	GTptt312	GTptt312_SGA10.1 GTptt312_SGA10.5 GTptt312_SGA20.1 GTptt312_SGA20.8 GTptt312_SGA5.1 GTptt312_SGA5.6 GTptt312_SGA5.7 GTptt312_SGA5.8 GTptt312_SGA2.6 (3.4kb cytB) GTptt312_SGA5.10 (3.4kb cytB)	=MEptt2520_SGA20.1 =BQptt392_SGA5.1(3.4Kb) =BQptt392_SGA5.1(3.4Kb) =BQptt392_SGA5.1(3.4Kb) =BQptt392_SGA5.1(3.4Kb) =BBptt238_SGA5.10(3.4Kb) =KApst382_SGA5.1(3.4Kb) =GTPtt312_SGA2.6(3.4Kb) =GTPtt312_SGA5.10(3.4Kb)	GTptt312_SGA2.6 GTptt312_SGA5.10	HM235279 HM235280	GTptt312_SGA5.9	HM235222					
25	GTptt314							GTptt314_SGA20.4 GTptt314_SGA20.7 GTptt314_SGA5.2 GTptt314_SGA5.5	=BBptt93_SGA10.1 HM235157 =UBpts1446_SGA5.5 HM235158			
26	GTptt503	GTptt503_SGA5.5 (3.4kb cytB) GTptt503_SGA5.8 (3.4kb cytB) GTptt503_SGA5.9 (3.4kb cytB)	=GTPtt503_SGA5.5(3.4Kb) =GTPtt503_SGA5.8(3.4Kb) =GTPtt503_SGA5.9(3.4Kb)	GTptt503_SGA5.5 GTptt503_SGA5.8 GTptt503_SGA5.9	HM235339 HM235340 HM235341	GTptt503_SGA5.4 GTptt503_SGA5.11	HM235223 =GTPtt503_SGA5.4	GTptt503_SGA2.1	HM235125			
27	GTptt514	GTptt514_SGA8.3 GTptt514_SGA8.5 GTptt514_SGA8.7	=GTPtt23_SGA10.8(3.4Kb) =GTPtt23_SGA10.8(3.4Kb) =GTPtt23_SGA10.8(3.4Kb)									
28	GTptt604	GTptt604_SGA5.2 (3.4kb cytB)	=GTPtt604_SGA5.2(3.4Kb)	GTptt604_SGA5.2	HM235336	GTptt604_SGA5.4	HM235224	GTptt604_SGA5.1	HM235139			



No	Sample	cytB	Accession No.	mtDNA-3.4kb SGA	Accession No.	mtDNA-3.3kb	Accession No.	ldh	Accession No.	cj/c	Accession No.		
45	BApts1375	BApts1373_SGA10.6	=BApts1405_SGA5.9(3.4Kb)										
		BApts1375_SGA5.1	=BFpts1171_SGA5.8(3.4Kb)										
		BApts1375_SGA5.2	=BApts1375_SGA10.7										
		BApts1375_SGA10.1	=BFpts1171_SGA5.8(3.4Kb)										
		BApts1375_SGA10.7	HM235108										
46	BApts1381	BApts1375_SGA20.1	=BFpts1171_SGA5.3(3.4Kb)										
		BApts1375_SGA20.5	=BApts1405_SGA5.9(3.4Kb)										
47	BApts1402	BApts1402_SGA5.10 (3.4kb cytB)	=BApts1402_SGA5.10(3.4Kb)	BApts1402_SGA5.10	HM235393								
48	BApts1405	BApts1405_SGA5.5 (3.4kb cytB)	=BApts1405_SGA5.5(3.4Kb)	BApts1405_SGA5.5	HM235395								
		BApts1405_SGA5.9 (3.4kb cytB)	=BApts1405_SGA5.9(3.4Kb)	BApts1405_SGA5.9	HM235396								
49	BApts1409	BApts1409_SGA5.1 (3.4kb cytB)	=BApts1409_SGA5.1(3.4Kb)	BApts1409_SGA5.1	HM235397								
50	BApts1413	BApts1413_SGA10.1	=BFpts1171_SGA5.3(3.4Kb)										
		BApts1413_SGA10.5	=BFpts1171_SGA5.3(3.4Kb)										
		BApts1413_SGA10.6	=CPttt584_SGA2.2(3.4Kb)										
		BApts1413_SGA10.9	=BApts1402_SGA5.10(3.4Kb)										
		BApts1413_SGA10.10	=BFpts1171_SGA5.3(3.4Kb)										
		BApts1413_SGA10.13	HM234976										
		BApts1413_SGA20.1	=BApts1405_SGA5.9(3.4Kb)										
		BApts1413_SGA20.6	=BFpts1171_SGA5.3(3.4Kb)										
		BApts1413_SGA20.9	=BApts1370_SGA2.9(3.4Kb)										
51	BFpts1169												
52	BFpts1170												
53	BFpts1171	BFpts1171_SGA5.3 (3.4kb cytB)	=BFpts1171_SGA5.3(3.4Kb)	BFpts1171_SGA5.3	HM235391	BFpts1171_SGA5.3	HM235181						
		BFpts1171_SGA5.7 (3.4kb cytB)	=BFpts1171_SGA5.7(3.4Kb)	BFpts1171_SGA5.7	HM235392	BFpts1171_SGA5.4	HM235182						
54	BFpts1172	BFpts1172_SGA5.8 (3.4kb cytB)	=BFpts1172_SGA5.8(3.4Kb)	BFpts1172_SGA5.8	HM235388	BFpts1172_SGA5.11	HM235389						
		BFpts1172_SGA5.11 (3.4kb cytB)	=BFpts1172_SGA5.11(3.4Kb)	BFpts1172_SGA5.11	HM235389	BFpts1171_SGA5.5	HM235183						
55	BFpts1534												
56	BFpts1541	BFpts1541_SGA2.1	=BApts1405_SGA5.9(3.4Kb)										
		BFpts1541_SGA5.1	=BFpts1171_SGA5.8(3.4Kb)										
57	Blpts2416	BFpts1541_SGA8.8	=BApts1405_SGA5.9(3.4Kb)										
58	EPpts899												
59	KApts1680	KApts1680_SGA3200.1	=KApts1680_SGA30.3(3.4Kb)	KApts1680_SGA30.3	HM235403	KApts1680_SGA300.1	HM235226	KApts1680_SGA20.1	=MTptt157_SGA5.6	EPpts899_SGA20.2	HM235166		
		KApts1680_SGA3200.2	=BApts1405_SGA5.9(3.4Kb)	KApts1680_SGA30.11	HM235404	KApts1680_SGA300.8	=KApts1680_SGA300.4	KApts1680_SGA20.3	=MTptt157_SGA5.6	KApts1680_SGA20.1	HM235166		
		KApts1680_SGA3200.5	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA3200.7	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA3200.8	HM235052										
		KApts1680_SGA3200.10	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA3200.11	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA3200.12	HM235049										
		KApts1680_SGA1600.2	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA1600.4	HM235051										
		KApts1680_SGA1600.5	HM235048										
		KApts1680_SGA1600.6	=KApts1680_SGA1600.4										
		KApts1680_SGA1600.9	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA1600.10	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA1600.11	=KApts1680_SGA3200.8										
		KApts1680_SGA1600.13	=BApts1405_SGA5.9(3.4Kb)										
		KApts1680_SGA800.1	=LUpts2074_SGA2.12(3.4Kb)										
		KApts1680_SGA800.3	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA800.11	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA800.13	=BApts1405_SGA5.9(3.4Kb)										
		KApts1680_SGA400.1	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA400.2	=KApts1680_SGA1600.4										
		KApts1680_SGA400.11	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA400.12	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA400.13	HM235080										
		KApts1680_SGA400.14	=BApts1405_SGA5.9(3.4Kb)										
		KApts1680_SGA160.2	=BApts1405_SGA5.9(3.4Kb)										
		KApts1680_SGA160.4	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA20.7	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA20.8	=BApts1405_SGA5.9(3.4Kb)										
		KApts1680_SGA30.3 (3.4kb cytB)	=KApts1680_SGA30.3(3.4Kb)										
		KApts1680_SGA30.11 (3.4kb cytB)	=KApts1680_SGA30.11(3.4Kb)										
		60	KApts1698										
61	KApts1674	KApts1674_SGA2.1	=BApts1375_SGA10.7										
		KApts1674_SGA20.2	=KApts1680_SGA30.3(3.4Kb)										
		KApts1674_SGA40.8	=CPttt584_SGA2.2(3.4Kb)										
		KApts1674_SGA5.1	=KApts382_SGA5.1(3.4Kb)										
		KApts1674_SGA5.2	=LUpts2074_SGA2.12(3.4Kb)										
62	KApts382	KApts1674_SGA8.4	=KApts382_SGA5.1(3.4Kb)										
		KApts1674_SGA8.7	=BApts1405_SGA5.9(3.4Kb)										
		KApts1674_SGA8.8	=BFpts1171_SGA5.3(3.4Kb)										
		KApts382_SGA5.1 (3.4kb cytB)	=KApts382_SGA5.1(3.4Kb)	KApts382_SGA5.1	HM235401								
		KApts382_SGA5.3 (3.4kb cytB)	=KApts382_SGA5.3(3.4Kb)	KApts382_SGA5.3	HM235402								
63	LUpts2074	LUpts2074_SGA2.11 (3.4kb cytB)	=LUpts2074_SGA2.11(3.4Kb)	LUpts2074_SGA2.11	HM235398								
		LUpts2074_SGA2.12 (3.4kb cytB)	=LUpts2074_SGA2.12(3.4Kb)	LUpts2074_SGA2.12	HM235399								
		LUpts2074_SGA2.13 (3.4kb cytB)	=LUpts2074_SGA2.13(3.4Kb)	LUpts2074_SGA2.13	HM235400								
64	LUpts2078	LUpts2078_SGA5.1 (3.4kb cytB)	=LUpts2078_SGA5.1(3.4Kb)	LUpts2078_SGA5.1	HM233319	LUpts2078_SGA5.2	HM235247						
		LUpts2078_SGA5.2 (3.4kb cytB)	=LUpts2078_SGA5.2(3.4Kb)	LUpts2078_SGA5.2	HM235320	LUpts2078_SGA5.8	HM235248						
						LUpts2078_SGA5.10	HM235245						
65	MUpts1086	MUpts1086_SGA20.6	HM235076										
		MUpts1086_SGA20.8	=BFpts1171_SGA5.3(3.4Kb)										
66	ONpts1321	ONpts1321_SGA5.1(3.4kb cytB)	=ONpts1321_SGA5.1(3.4Kb)	ONpts1321_SGA5.1	HM235387								
67	ONpts1345												
68	UBpts1446												
70	VMpte11												
71	VMpte12	VMpte11_SGA20.1	HM235083										
		VMpte11_SGA20.4	=BQptt392_SGA5.1(3.4Kb)										
		VMpte11_SGA10.2	=BQptt392_SGA5.1(3.4Kb)										
		VMpte11_SGA10.5	=BQptt392_SGA5.1(3.4Kb)										
		VMpte11_SGA10.13	HM235082										
		VMpte11_SGA5.2	HM235084										
		VMpte11_SGA5.3	=BQptt392_SGA5.7(3.4Kb)										
		VMpte11_SGA5.5	HM235085										
		VMpte11_SGA5.6	=BQptt392_SGA5.1(3.4Kb)										
		VMpte11_SGA5.7	=DPptt160_SGA5.5										
		VMpte11_SGA5.8	=BBptt238_SGA5.10(3.4Kb)										
		VMpte11_SGA5.13	=BQptt392_SGA5.1(3.4Kb)										
			HM235086										



No	Sample	cytB	Accession No.	mtDNA-3.4kb SGA	Accession No.	mtDNA-3.3kb	Accession No.	ldh	Accession No.	cj/c	Accession No.	
12	DPgor1144	DPgor1144_SGA5.7 DPgor1144_SGA10.6	=Ggor82_SGA5.1(3.4Kb) =DTgor2_SGA5.1(3.4Kb)									
13	DSgor24	DSgor24_SGA10.5 DSgor24_SGA10.8 DSgor24_SGA10.9 DSgor24_SGA20.4 DSgor24_SGA20.12 DSgor24_SGA5.1 (3.4kb cytB) DSgor24_SGA5.6 (3.4kb cytB) DSgor24_SGA5.11 (3.4kb cytB) DSgor24_SGA5.12 (3.4kb cytB) DSgor24_SGA5.13 (3.4kb cytB)	=DSgor24_SGA5.12(3.4Kb) =DSgor24_SGA5.12(3.4Kb) <b>HM234998</b> =DSgor24_SGA5.12(3.4Kb) =DSgor24_SGA5.12(3.4Kb) =DSgor24_SGA5.1(3.4Kb) =DSgor24_SGA5.6(3.4Kb) =DSgor24_SGA5.1(3.4Kb) =DSgor24_SGA5.12(3.4Kb) =DSgor24_SGA5.13(3.4Kb)	DSgor24_SGA5.1 DSgor24_SGA5.6 DSgor24_SGA5.11 DSgor24_SGA5.12 DSgor24_SGA5.13	HM235294 HM235295 =DSgor24_SGA5.1 HM235290 HM235291					DSgor24_SGA2.3 DSgor24_SGA2.8	HM235154 =DSgor24_SGA2.3	
14	DSgor30							DSgor30_SGA1.1	HM235143			
15	DSgor36	DSgor36_SGA10.1 DSgor36_SGA10.2 DSgor36_SGA10.5 DSgor36_SGA10.12	=BQgor58_SGA5.2(3.4Kb) =BQgor58_SGA5.2(3.4Kb) =BQgor58_SGA5.2(3.4Kb)									
16	DSgor38	DSgor38_SGA2.2 DSgor38_SGA2.7 DSgor38_SGA2.8 DSgor38_SGA5.2 DSgor38_SGA5.7 DSgor38_SGA20.7	=DSgor38_SGA5.7 <b>HM235000</b> =DSgor38_SGA5.7 <b>HM235002</b> <b>HM235003</b> <b>HM235001</b>							DSgor38_SGA2.3	HM235155 =GTgor34_SGA5.4	
17	DSgor54	DSgor54_SGA10.2 DSgor54_SGA5.1 (3.4kb cytB) DSgor54_SGA5.2 (3.4kb cytB)	=DSgor24_SGA5.12(3.4Kb) =DSgor54_SGA5.1(3.4Kb) =DSgor54_SGA5.2(3.4Kb)	DSgor54_SGA5.1 DSgor54_SGA5.2	HM235312 =DSgor24_SGA5.1	DSgor54_SGA5.2 DSgor54_SGA5.3	=GTgor119_SGA300.3 =GTgor119_SGA300.3					
18	DSgor60	DSgor60_SGA20.7	=DSgor64_SGA10.1									
19	DSgor64	DSgor64_SGA10.1 DSgor64_SGA10.5	=DSgor64_SGA10.1									
20	DSgor86	DSgor86_SGA5.1(3.4kb cytB) DSgor86_SGA5.5(3.4kb cytB)	=DSgor86_SGA5.1(3.4Kb) =DSgor86_SGA5.5(3.4Kb)	DSgor86_SGA5.1 DSgor86_SGA5.6	HM235292 HM235311	DSgor86_SGA2.1 DSgor86_SGA2.3 DSgor86_SGA2.4 DSgor86_SGA2.12 DSgor86_SGA5.5	HM235201 HM235202 HM235203 =DSgor86_SGA2.1 HM235204					
21	EKgor1179	EKgor1179_SGA10.8 EKgor1179_SGA10.9 EKgor1179_SGA160.1 EKgor1179_SGA160.9 EKgor1179_SGA20.6 EKgor1179_SGA320.4 EKgor1179_SGA320.6 EKgor1179_SGA320.8 EKgor1179_SGA40.2 EKgor1179_SGA40.3 EKgor1179_SGA40.4 EKgor1179_SGA40.9 EKgor1179_SGA40.10 EKgor1179_SGA80.2 EKgor1179_SGA80.4 EKgor1179_SGA80.6 EKgor1179_SGA80.7	<b>HM235004</b> <b>HM235005</b> <b>HM235006</b> <b>HM235007</b> =Ggor82_SGA5.1(3.4Kb) =Mlgor1542_SGA10.2 =GTgor2_SGA5.1(3.4Kb) =GTgor2_SGA5.1(3.4Kb) <b>HM235008</b> <b>HM235009</b> <b>HM235010</b> <b>HM235011</b> =GTgor2_SGA5.1(3.4Kb) =GTgor2_SGA5.1(3.4Kb) <b>HM235012</b> <b>HM235013</b> =GTgor2_SGA5.1(3.4Kb)									
22	EKgor1182	EKgor1182_SGA10.1 EKgor1182_SGA10.2 EKgor1182_SGA10.3 EKgor1182_SGA10.6 EKgor1182_SGA10.7 EKgor1182_SGA5.1 EKgor1182_SGA5.4 EKgor1182_SGA5.9	<b>HM235014</b> =Lbgor1222_SGA20.5(3.4Kb) =GTgor2_SGA5.1(3.4Kb) <b>HM235015</b> =Bbgor228_SGA5.2(3.4Kb) =GTgor2_SGA5.1(3.4Kb) <b>HM235016</b> <b>HM235017</b>									
23	EKgor1183	EKgor1183_SGA20.1	=GTgor82_SGA5.1(3.4Kb)									
24	GTgor6	GTgor6_SGA10.11 GTgor6_SGA20.6	=Lbgor1222_SGA20.5(3.4Kb) =Bbgor228_SGA5.6(3.4Kb)									
25	GTgor8	GTgor8_SGA20.4 GTgor8_SGA20.6 GTgor8_SGA20.10 GTgor8_SGA20.11 GTgor8_SGA20.12 GTgor8_SGA20.2 GTgor8_SGA10.2 GTgor8_SGA10.10	<b>HM235042</b> =GTgor8_SGA5.1(3.4Kb) =GTgor8_SGA5.1(3.4Kb) <b>HM235039</b> =GTgor8_SGA20.4 =GTgor8_SGA20.4 <b>HM235038</b> =Bbgor228_SGA5.6(3.4Kb) <b>HM235034</b> <b>HM235035</b> =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =GTgor10_SGA2.2(3.4Kb) =NDgor3203_SGA5.2(3.4Kb) =GTgor10_SGA2.11(3.4Kb) =GTgor10_SGA2.12(3.4Kb) =GTgor10_SGA2.14(3.4Kb) =GTgor10_SGA2.20(3.4Kb) =GTgor10_SGA2.21(3.4Kb) =GTgor10_SGA2.24(3.4Kb)									
26	GTgor10	GTgor10_SGA10.4 GTgor10_SGA10.6 GTgor10_SGA20.10 GTgor10_SGA5.2 GTgor10_SGA5.3 GTgor10_SGA5.8 GTgor10_SGA5.10 GTgor10_SGA2.2 (3.4kb cytB) GTgor10_SGA2.6 (3.4kb cytB) GTgor10_SGA2.11 (3.4kb cytB) GTgor10_SGA2.12 (3.4kb cytB) GTgor10_SGA2.14 (3.4kb cytB) GTgor10_SGA2.20 (3.4kb cytB) GTgor10_SGA2.21 (3.4kb cytB) GTgor10_SGA2.24 (3.4kb cytB)	=Bbgor228_SGA5.6(3.4Kb) <b>HM235034</b> <b>HM235035</b> =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =GTgor10_SGA2.2(3.4Kb) =NDgor3203_SGA5.2(3.4Kb) =GTgor10_SGA2.11(3.4Kb) =GTgor10_SGA2.12(3.4Kb) =GTgor10_SGA2.14(3.4Kb) =GTgor10_SGA2.20(3.4Kb) =GTgor10_SGA2.21(3.4Kb) =GTgor10_SGA2.24(3.4Kb)	GTgor10_SGA2.2 GTgor10_SGA2.6 GTgor10_SGA2.11 GTgor10_SGA2.12 GTgor10_SGA2.14 GTgor10_SGA2.20 GTgor10_SGA2.21 GTgor10_SGA2.24	HM235270 =NDgor3203_SGA5.2 HM235273 HM235274 HM235275 HM235272	GTgor10_SGA2.1 GTgor10_SGA2.5 GTgor10_SGA2.9 GTgor10_SGA2.12 GTgor10_SGA2.14 GTgor10_SGA2.18 GTgor10_SGA2.19 GTgor10_SGA2.20 GTgor10_SGA2.26 GTgor10_SGA2.27 GTgor10_SGA2.28	HM235205 HM235209 HM235210 HM235210 HM235206 HM235207 =GTgor10_SGA2.9 HM235208 =GTgor10_SGA2.9 =GTgor10_SGA2.5 =GTgor10_SGA2.9	GTgor10_SGA2.19 GTgor10_SGA2.23	HM235119 HM235120	GTgor10_SGA5.6 GTgor10_SGA5.7 GTgor10_SGA2.6 GTgor10_SGA2.8	=GTgor84_SGA2.1 =GTgor84_SGA2.1 =GTgor84_SGA2.1 =GTgor84_SGA2.1	
27	GTgor26	GTgor26_SGA20.1	=GTgor34_SGA5.10(3.4Kb)	GTgor34_SGA5.10	HM235365	GTgor34_SGA2.9	HM235217			GTgor26_SGA2.1	=BQgor34_SGA2.1	
28	GTgor34	GTgor34_SGA10.3 GTgor34_SGA10.11 GTgor34_SGA5.10 (3.4kb cytB) GTgor34_SGA5.23 (3.4kb cytB)	=GTgor34_SGA5.10(3.4Kb) =GTgor34_SGA5.10(3.4Kb) =GTgor34_SGA5.10(3.4Kb) =GTgor34_SGA5.23(3.4Kb)	GTgor34_SGA5.10 GTgor34_SGA5.23	HM235365 HM235308					GTgor34_SGA5.4	HM235164	
29	GTgor68	GTgor68_SGA10.3	=GTgor34_SGA5.10(3.4Kb)									
30	GTgor82	GTgor82_SGA5.1 (3.4kb cytB) GTgor82_SGA5.4 (3.4kb cytB) GTgor82_SGA5.7 (3.4kb cytB) GTgor82_SGA5.8 (3.4kb cytB) GTgor82_SGA5.10 (3.4kb cytB)	=GTgor82_SGA5.1(3.4Kb) =GTgor82_SGA5.4(3.4Kb) =GTgor82_SGA5.7(3.4Kb) =GTgor82_SGA5.8(3.4Kb) =GTgor82_SGA5.10(3.4Kb)	GTgor82_SGA5.1 GTgor82_SGA5.4 GTgor82_SGA5.7 GTgor82_SGA5.8 GTgor82_SGA5.10	HM235371 HM235372 HM235373 HM235374 HM235375							
31	GTgor84	GTgor84_SGA10.1 GTgor84_SGA10.2 GTgor84_SGA10.3 GTgor84_SGA10.4 GTgor84_SGA20.9 GTgor84_SGA20.11 GTgor84_SGA20.12 GTgor84_SGA5.5 (3.4kb cytB)	=Bbgor228_SGA5.6(3.4Kb) <b>HM235040</b> =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb) =Bbgor228_SGA5.6(3.4Kb)	GTgor84_SGA5.5	HM235314 HM235315 HM235316 HM235317 HM235318 HM235319	GTgor84_SGA5.1 GTgor84_SGA5.11	HM235218 HM235220	GTgor84_SGA5.1 GTgor84_SGA5.2 GTgor84_SGA2.2 GTgor84_SGA2.4 GTgor84_SGA2.5 GTgor84_SGA2.6	=GTgor84_SGA2.1 =GTgor84_SGA2.1 =GTgor84_SGA2.1 =GTgor84_SGA2.1 =GTgor84_SGA2.1 =GTgor84_SGA2.1			
32	GTgor85							GTgor85_SGA1.1	HM235142			
33	GTgor89	GTgor89_SGA5.5 GTgor89_SGA5.13 GTgor89_SGA10.2	=Bbgor228_SGA5.6(3.4Kb) <b>HM235041</b> =Bbgor228_SGA5.2(3.4Kb)									
34	GTgor96	GTgor96_SGA10.3 GTgor96_SGA10.7 GTgor96_SGA10.9 GTgor96_SGA10.11 GTgor96_SGA10.12 GTgor96_SGA10.13 GTgor96_SGA20.2 GTgor96_SGA20.5 GTgor96_SGA20.6 GTgor96_SGA20.11	=Bbgor228_SGA5.2(3.4Kb) <b>HM235044</b> <b>HM235045</b> =GTgor82_SGA5.1(3.4Kb) =Bbgor228_SGA5.2(3.4Kb) <b>HM235043</b> =Lbgor1222_SGA20.5(3.4Kb) =Lbgor1222_SGA20.5(3.4Kb) =Bbgor228_SGA5.2(3.4Kb) =Bbgor228_SGA5.2(3.4Kb)							GTgor96_SGA40.2	=BQgor34_SGA2.1	
35	GTgor118	GTgor118_SGA40.3 GTgor118_SGA40.4 GTgor118_SGA80.9 GTgor118_SGA20.3 (3.4kb cytB)	=GTgor82_SGA5.1(3.4Kb) =GTgor118_SGA20.4(3.4Kb) =Lbgor1222_SGA20.5(3.4Kb) =GTgor118_SGA20.3(3.4Kb)	GTgor118_SGA20.3 GTgor118_SGA20.4 GTgor118_SGA20.12	HM235369 HM235370 =GTgor118_SGA20.4	GTgor118_SGA20.1 GTgor118_SGA20.2 GTgor118_SGA20.3 GTgor118_SGA20.7	HM235211 HM235212 HM235213 HM235214	GTgor118_SGA2.7 HM235128	GTgor118_SGA10.4	=GTgor84_SGA2.1		





**Supplementary Table 7. GenBank accession numbers of previously published *Plasmodium* sequences**

Strain	<i>cytB</i>	mtDNA-3.4kb	mtDNA-3.3kb	<i>ldh</i>	<i>clpC</i>
<i>P. falciparum</i> _102-1	AY282924		AY282924		
<i>P. falciparum</i> _124-8		AY282926			
<i>P. falciparum</i> _128-4			AY282927		
<i>P. falciparum</i> _1917	AY282929				
<i>P. falciparum</i> _3D7			AY282930 <sup>b</sup>	AL844509	
<i>P. falciparum</i> _418			AY282932		
<i>P. falciparum</i> _449			AY282936		
<i>P. falciparum</i> _7G8	AJ276847				
<i>P. falciparum</i> _9021	AY282947				
<i>P. falciparum</i> _D5			AY282951 <sup>c</sup>		
<i>P. falciparum</i> _FCC1/HN				AF323520	
<i>P. falciparum</i> _FCC1/HN				DQ825436	
<i>P. falciparum</i> _HZ357		AY282963			
<i>P. falciparum</i> _I1	AY588279				
<i>P. falciparum</i> _I2	AY588280				
<i>P. falciparum</i> _I3	AY910012				
<i>P. falciparum</i> _I4	AY910013				
<i>P. falciparum</i> _IGH-CR14			ACBS01001974		
<i>P. falciparum</i> _IR-B					X95276
<i>P. falciparum</i> _JCK			AY282972 <sup>d</sup>		
<i>P. falciparum</i> _Jind				EU330208	
<i>P. falciparum</i> _LDH-P				AF251291	
<i>P. falciparum</i> _LF4-1	AY282975				
<i>P. falciparum</i> _M2		AY282977			
<i>P. falciparum</i> _Malay Camp		M99416 <sup>a</sup>	M99416 <sup>e</sup>		
<i>P. falciparum</i> _P98-11			AY282984		
<i>P. falciparum</i> _PNG9-1	AY283003				
<i>P. falciparum</i> _REN			AY283005		
<i>P. falciparum</i> _TDD060320				EU589948	
<i>P. falciparum</i> _TDD060367				EU589947	
<i>P. falciparum</i> _Tha16			AY283009 <sup>f</sup>		
<i>P. falciparum</i> _TM191c			AY283016		
<i>P. knowlesi</i> _H				XM_002260056	
<i>P. knowlesi</i> _Malayan					AB471880
<i>P. knowlesi</i> _Malayan MRA-487	AY722797	AY722797	AY722797		
<i>P. malariae</i>	AB354570	AB354570	AB354570		AF348342
<i>P. malariae</i> _Uganda I				AY486059	
<i>P. ovale</i>	AB354571	AB354571	AB354571		AY634623
<i>P. ovale</i> _Harding				AY486058	
<i>P. vivax</i> _ASA06R09632				EU589957	
<i>P. vivax</i> _Belem					AB471871
<i>P. vivax</i> _pvSO2	AY598117	AY598117	AY598117		
<i>P. cynomolgi</i>	AY800108	AB434919	AB434919		
<i>P. cynomolgi</i> _Ceylonensis					AB471873
<i>P. fragile</i>	AY722799	AY722799	AY722799		
<i>P. fragile</i> _Hackeri					AB471876
<i>P. gonderi</i>	AB434918	AB434918	AB434918		
<i>P. gonderi</i> _ATCC30045					AB471877
<i>P. inui</i>	AB354572	AB354572	AB354572		
<i>P. inui</i> _Celebes					AB471879
<i>P. reichenowi</i>	AJ251941	AJ251941	AJ251941		
<i>P. reichenowi</i> _Oscar				AB122147	
<i>P. simiovale</i>	AB434920	AB434920	AB434920		
<i>P. simiovale</i> _ATCC30140					AB471881
<i>P. simium</i>	AY800110	AY800110	AY800110		
<i>P. ovale</i> _variant (Duval '09)	FJ409566				
CPZcam89 (Duval '09)	FJ409565				
CPZcam91 (Duval '09)	FJ409564				
<i>P. gaboni</i> _K (Ollomo)	FJ895307	FJ895307	FJ895307		
Bana (Rich)	EU560453				EU560463
Gabon (Rich)	EU560466				
Loukoum (Rich)	EU560459				EU560462
Max (Rich)	EU560455				EU560465
Dibamba (Rich)	EU560457				
Nino (Rich)	EU560454				EU560464
Rafiki 1 (Rich)	EU560456				EU560461
Rafiki 2 (Rich)	EU560458				EU560460
MB753 (Prugnonle)	GU045318				

Strain	<i>cytB</i>	mtDNA-3.4kb	mtDNA-3.3kb	<i>ldh</i>	<i>clpC</i>
MB783 (Prugnonle)	GU045319				
MP1309 (Prugnonle)	GU045314				
sgGOmoeb (Prugnonle)	GU045312				
TK060 (Prugnonle)	GU045313				
BQ2341 (Prugnonle)	GU045316				
BQ2367 (Prugnonle)	GU045320				
BQ638 (Prugnonle)	GU045322				
BQ642 (Prugnonle)	GU045315				
BQ654 (Prugnonle)	GU045311				
BQ668 (Prugnonle)	GU045317				
CP1426 (Prugnonle)	GU045321				
DRC_A (Krief)	GQ355474	GQ355474	GQ355474		
DRC_C (Krief)	GQ355473	GQ355473	GQ355473		
DRC_E (Krief)	GQ355472	GQ355472	GQ355472		
DRC_G (Krief)	GQ355480				
DRC_I (Krief)	GQ355479				
DRC_J (Krief)	GQ355486				
DRC_L (Krief)	GQ355475	GQ355475	GQ355475		
DRC_Q (Krief)	GQ355485				
DRC_S1 (Krief)	GQ355468				
DRC_S2 (Krief)	GQ355469				
DRC_S3 (Krief)	GQ355476	GQ355476	GQ355476		
UG_B1 (Krief)	GQ355470				
UG_B2 (Krief)	GQ355481				
UG_D1 (Krief)	GQ355471				
UG_D2 (Krief)	GQ355477				
UG_F (Krief)	GQ355478				
CPZcam46 (Duval '10)	HM000107				
CPZcam61 (Duval '10)	HM000108				
CPZcam80 (Duval '10)	HM000109				
CPZcam83 (Duval '10)	HM000110				
CPZcam137 (Duval '10)	HM000111				
CPZcam155 (Duval '10)	HM000112				
GGcam10 (Duval '10)	HM000105				
GGcam13 (Duval '10)	HM000106				
LLLD2010/Lemur (Duval '10)	HM000113				

<sup>a</sup>Represents haplotype shared by 101 additional human *P. falciparum* sequences as shown in Fig. 3a: 102-1 (AY282924), 123-5 (AY282925), 128-4 (AY282927), 1905 (AY282928), 1917 (AY282929), 3D7 (AY282930), 413-1 (AY282931), 418 (AY282932), 425 (AY282933), 433 (AY282934), 434 (AY282935), 449 (AY282936), 569-1 (AY282937), 569-2 (AY282938), 569-3 (AY282939), 596-1 (AY282940), 596-2 (AY282941), 601 (AY282942), 713 (AY282943), 7G8 (AJ276847), 9013 (AY282944), 9016 (AY282945), 9020 (AY282946), 9021 (AY282947), C2A (AY282948), CAMP (AY282949), D10 (AY282950), D5 (AY282951), Dd2 (AY282952), DIV14 (AY282953), DIV17 (AY282954), DIV30 (AY282955), ECP (AY282956), ECU (AY282957), FAB6 (AY282958), FAB9 (AY282959), NC\_002375, FCB (AY282960), Haiti (AY282961), Hb3 (AY282962), HB3 (DQ642845), HZ395 (AY282964), HZ475 (AY282965), HZ529 (AY282966), HZ597 (AY282967), HZ945 (AY282968), ICS (AY282969), Indo (AY282970), JAV (AY282971), JCK (AY282972), K1 (AJ276845), K39 (AY282973), KMVII (AY282974), LF4-1 (AY282975), M190 (AY282976), M24 (AY282978), M5 (AY282979), M76611, M97 (AY282980), MTs-1 (AY282981), NF54 (AJ276844), P13 (AY282982), P31 (AY282983), P98-11 (AY282984), P98-13 (AY282985), P98-18 (AY282986), P98-4 (AY282987), P98-5 (AY282988), P99-1 (AY282989), P99-3 (AY282990), PAD (AY282991), PC09 (AY282992), PC15 (AY282993), PC17 (AY282994), PC26 (AY282995), PC49 (AY282996), PNG10-1 (AY282997), PNG13 (AY282998), PNG2 (AY282999), PNG3 (AY283000), PNG4 (AY283001), PNG5-1 (AY283002), PNG9-1 (AY283003), PNG9-3 (AY283004), RAJ116 (ACBR01002728), REN (AY283005), S35 (AY283006), SLD6 (AY283007), T2c6 (AY283008), T9-96 (AJ276846), Tha16 (AY283009), Tha17-1 (AY283010), Tha18-1 (AY283011), Tha18-2 (AY283012), Tha19 (AY283013), Tha2-1 (AY283014), Tha2-2 (AY283015), TM191c (AY283016), TM284 (AY283017), V1S (AY283018), WR80 (AY283019).

<sup>b</sup>Represents haplotype shared by 1 additional human *P. falciparum* sequences as shown in Fig. 3b: NF54 (AJ276844).

<sup>c</sup>Represents haplotype shared by 15 additional human *P. falciparum* sequences as shown in Fig. 3b: Dd2 (AY282952), FCB (AY282960), Indo (AY282970), JAV (AY282971), K1 (AJ276845), M76611, P31 (AY282983), P98-13 (AY282985), P98-4 (AY282987), P98-5 (AY282988), Tha19 (AY283013), Tha2-1 (AY283014), Tha2-2 (AY283015), V1S (AY283018), WR80 (AY283019).

<sup>d</sup>Represents haplotype shared by 1 additional human *P. falciparum* sequences as shown in Fig. 3b: TM284 (AY283017).

<sup>e</sup>Represents haplotype shared by 73 additional human *P. falciparum* sequences as shown in Fig. 3b: 123-5 (AY282925), 124-8 (AY282926), 1905 (AY282928), 1917 (AY282929), 413-1 (AY282931), 425 (AY282933), 433 (AY282934), 434 (AY282935), 596-1 (AY282940), 596-2 (AY282941), 569-3 (AY282939), 596-1 (AY282940), 596-2 (AY282941), 601 (AY282942), 713 (AY282943), 7G8 (AJ276847), 9013 (AY282944), 9016 (AY282945), 9020 (AY282946), 9021 (AY282947), C2A (AY282948), CAMP (AY282949), D10 (AY282950), DIV14 (AY282953), DIV17, (AY282954), DIV30 (AY282955), ECP (AY282956), ECU (AY282957), FAB6 (AY282958), FAB9 (AY282959), Haiti (AY282961), Hb3 (AY282962), HB3 (DQ642845), HZ357 (AY282963), HZ395 (AY282964), HZ475 (AY282965), HZ529 (AY282966), HZ597 (AY282967), HZ945 (AY282968), ICS (AY282969), K39 (AY282973), KMVII (AY282974), LF4-1 (AY282975), M190 (AY282976), M2 (AY282977), M24 (AY282978), M5 (AY282979), M97 (AY282980), MTs-1 (AY282981), P13 (AY282982), P98-18 (AY282986), P99-1 (AY282989), P99-3 (AY282990), PAD (AY282991), PC09 (AY282992), PC15 (AY282993), PC17 (AY282994), PC26 (AY282995), PC49 (AY282996), PNG10-1 (AY282997), PNG13 (AY282998), PNG2 (AY282999), PNG3 (AY283000), PNG4 (AY283001), PNG5-1 (AY283002), PNG9-1 (AY283003), PNG9-3 (AY283004), RAJ116 (ACBR010027), S35 (AY283006), SLD6 (AY283007), T2c6 (AY283008), T9-96 (AJ276846), Tha17-1 (AY283010).

<sup>f</sup>Represents haplotype shared by 2 additional human *P. falciparum* sequences as shown in Fig. 3b: Tha18-1 (AY283011), Tha18-2 (AY283012).